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GenCore version 5.1.3
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February 10, 2003, 10:53:38; Search time 6264.22 Seconds (without alignments) 11470.669 Million cell updates/sec US-09-610-313-30 2469 1 gtcgacgccaccatggccga......gggctagcaccggtgaattc 2469 4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Title: Perfect score: Sequence: Scoring table: Searched: Run on;

Database :

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ALIGNMENTS

PAT 06-JUL-2002 zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensburg,E.
Polymuclectidess encoding antigenic hiv type c polypeptides,
polypeptides and uses thereof
Patent: Wo 0204493-A 30 17-JAN-2002; linear DNA Sequence 30 from Patent W00204493. AX455914 AX455914.1 GI:21714899 synthetic construct. synthetic construct artificial sequences. RESULT 1
AX455914
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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Location/Qualifiers

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| | CCGCCCACAAGGGCATCGGCGGCACCGCCCCCCACAAGGCCATCGGCGGCACCCCCCACAAGGCCATCGGCGGCACGCCCCCCACAGGCCATCGGCGCCCCCCCC | AX455915 AX455915 AX455915.1 CI:2171490 Synthetic construct. Synthetic construct. artificial sequences. I zur Megede,J., Barnett Polynucleotides encodi polypeptides and uses Patent:WO 0204493.A CHIRON CORPORATION (US Location/Qual 1. 2467.A //ODSANTER="EXA/ADE."Sy/ADE." | Match 98 9%; Scales Samilarity 99.6%; Procal Similarity 99.6%; Procal Similarity 99.6%; Procal Similarity 99.6%; Procal Similarity 99.6%; Procange 1 Greacecaececargececaececaececaececaececae |
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| Db 1201 GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGC 1254 | QY 1441 ATCCAGAAGCTGGTGGCCAAGCTGAACTGGGCCAGCCAGTCTACCCCGGCATCAAGGTG 1500 HIRTHITHITHITHITHITHITHITHITHITHITHITHITHIT | QY 1681 TGGACCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG 1740 Db 1675 TGGACTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG 1734 QY 1741 ATGCGCACCGCCCACCACCAACGACGTGAAGCAGCTGACGAGGCCGTGCAAAGATCGCC 1800 Db 1735 ATGCGCACCGCCCACACGACGACGTGAAGCAGCTGACGAGGCCGTGCAAAGATCGCC 1800 Db 1735 ATGCGCCACCGCCCAACGACGTGAAGCTGACCGACGCCGTGCCTGCAGAAGATCGCC 1794 | QY 1801 ATGGAGAGCATCGTGGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCCATCCAGAAGGG 1860 Db 1795 ATGGAGAGCATCGTGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGA 1854 QY 1861 ACCTGGGAGACCTGGTGACCGACTTCGCAGCTGGATCCCCGAGTGGGAGTTC 1920 Db 1855 ACCTGGGAGACCTGGTGGACCGACTACTGGAGCCCCCTGGATCCCCGAGTGGGAGTTC 1920 Db 1855 ACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTC 1914 | 1921 GTGAACACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGC 198 | QY 2041 TACGTGACCGGCCGGCGGCAGAAGATCGTGACCCTACCGACACCACAGAAG 2100 Db 2035 TACGTGACCGGGCCGCGCAGAAGATCGTGAGCCTGACCGAGACCACCAGAAG 2094 QY 2101 ACCGAGCTGCAGCCTCCAGCTGGCCTGCAGGACACGAGGTGAACATCGTG 2160 Db 2095 ACCGAGCTGCAGCCATCCAGCTGCCCTGCAGGACAGCGAGGTGAACATCGTG 2160 Db 2095 ACCGAGCTGCAGCCATCCAGCTGCAGGACAGCGAGCGAGGTGAACATCGTG 2154 | Oy 2161 ACCGACAGCCAGGCCATGATCCAGGCCCAGCAGCAGGGGGGGG |
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          ATGCGCACCGCCCACAACCAACGAGCTGAAGCTGACCGAGGCCGTGCAGAAGATCGCC
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                           Huang,Y. and Nabel,G.J. Modifications of hiv env, gag, and pol enhance immunogenicity
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                                                                                                                                                 83.1%; Score 2051.2; DB 6; Length 9166;
llarity 92.6%; Pred. No. 6.6e-207;
Conservative 0; Mismatches 163; Indels 13;
                                                                                          25-APR-2002;
STATES (US)
                                                                         Location/Qualifiers
1. .9166
                                                      Patent: WO 0232943-A 168
GOVERNMENT OF THE UNITED
                                             genetic immunization
synthetic construct artificial sequences
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CCGCCGCCTGAAGAAGAAGAAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTCA
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                                                                                          3980 GCGTGCCCTGGACAAGGACTTCCGCAAGTACACCGCCTTCACCATCACCAGCATCAACA
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 CCTGGGAGGCCTGGTGGACCGAGTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG
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                                      CCGAGACCTTCTACGTGGACGCCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCT
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Pred. No. 5e-206;
0; Mismatches 177; Indels
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Patent: WO 0232943-A 174 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
1. 9788
1. 9788
//organism="synthetic construct"
//db xref="taxon:32630"
/note="plasmid pVR1012x/s contain.
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Modifications of hiv env, gag, and pol
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Best Local Similarity 91.8%;
Matches 2197; Conservative
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| Qy | 1322 | CCGACAAGAAGCACCAGAAGGACCCCCTTCCTGGGATGGGCTACGAGCTGCACCCCG 1381 |
| Qy | 1382 | ACAAGIGGACCGIGCAGCCCATCGAGCTGCCCGAGAGGAGAG |
| Qy | 1442 | TCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGC 1501 |
| Qy Db | 1502 | GCCAGCTGTGCAAGCTGCTGCGCGCGCGAAGGCCCTGACCGACATCGTGCCCCTGACCG 1561 |
| Qy Db | 1562 | AGGAGCCCGAGCTGGAGCTGGCCGAGAACCGCGGAGATCCTGCGCGGGCCCGTGCACGCC 1621 |
| Oy Db | 1622 | TGTACTACGACCCGAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGCCCACGACCAGT 1681 |
| Qy | 1682 | GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGA 1741 |
| Qy | 1742 | TGCGCACCGCCACAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA 1801 |
| Qy | 1802 | TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA 1861 |
| Qy | 1862 4815 | CCTGGGAGACCTGGTGGACCGACTACTGGCAGCCACCTGGATCCCCGAGTGGGAGTTCG 1921 |
| Qy | 1922 4875 | TGAACACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAGGAGCCCATCATCGGCG 1981 |
| Qy Db | 1982 4935 | CCGAGACCTICTACGIGGACGCGCGCCAACCGCGAGCCAAGAICGGCAAGGCCGGCT 2041 |
| Qy Db | 2042 4995 | ACGTGACCGACCGGGCCGGCAGAAGATCGTGACCTGACC |
| Qy Db | 2102 5055 | CCGAGCTGCAGCCATCCAGCTGGCCCTGCAGGACGAGCGAG |
| Qy | 2162 | CCGACAGCAGTACGCCCTGGGCATCATCCAGGCCCAGCAGAAGAGCGAGC |
| Qy | 2222 5175 | TGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGC 2281 |
| Oy Db | 2282 5235 | CCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCC 2341 |

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PAT 20-JUN-2002
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0232943-A 169 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
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1. 9169

Aorganism="synthetic construct"

/db_xref="taxon:32630"

/note="plasmid pVR1012x/s containing HIV genes"

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Sequence 169 from Patent WO0232943.
AX427931
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Best Local Similarity 91.7%;
Matches 2194; Conservative (
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                                                                                                  GCGTGCCCCTGGACGACGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACA
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 TGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCAGCTGGGCTGCA
                                           CCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG
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Modifications of hiv env, gag, and pol
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| Local Similarity nes 2194; Conser | 14 TGG(| | | 191 TGAN 3147 TGAN | 251 GCAJ 206 GGAJ | 311 TGC/ 266 TTC/ | 365 | 419 TGGC 1 | 479 AGA1 3446 AGA1 | 539 AGG1 506 AGG1 | 599 TGC1 566 TGC1 | 659 GCAC 3626 GCAC | 719 TGG 3686 TGG | 779 CCA1 3746 AGA1 | 839 ACAA 3806 ACAA | 899 ACTT 3866 ACTT | | 1019 TCAG |
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                                  AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGTTCGGCGGCTTCATCA
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Pred. No. 3.4e-204;
0; Mismatches 186;
                                                                             /organism="synthetic construct"
/db_xref="taxon:32630"
/note="plasmid pVR1012x/s conta
  env, gag, and pol
Modifications of hiv env, gag, and pogenetic immunization
Patent: WO 0232943-A 164 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
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                                                      ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA
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                                1979 GCGCCGAGACCTTCTACGTGGACGGCGCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
                                                                                                     GCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACAACCAGA
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Modifications of hiv env, gag, and pol
genetic immunization
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Modifications of hiv env, gag, and pol
genetic immunication
150 232943-A 159 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
LOCATION/QUALIFIERS
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Patent: WO 0232943-A 171 25-APR-2002;
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                                                              TCCGCAACCAGCGCAAGATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACACCGCCC
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                                                                                                                                            TGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG
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                                    TCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCC
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| DP OY OP | 03 113 115 115 | CAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCCA 409 CCCCAGCATCTTCCAGAGCAGCATCACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC 119 |
|----------------|-------------------------|--|
| Db Qy Db | 15 25 21 | |
| Qy Dp | 1319 | CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGCCTACGAGCTCCACC 1378 |
| oy Oy | 1379 | CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACG 1438 |
| ογ Db | 1439 | ACATCCAGAAGCTGGTGGCAACCTGAACTGGGCCAGCCAG |
| Qy Dp | 1499 | TGCGCCAGCTGTGCAAGCTGCTGCGGGGCCCAAGGCCCTGACCGACATCGTGCCCCTGA 1558 |
| Qy | 1559 4518 | CCGAGGAGCCCAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG 1618 |
| Qy Dp | 1619 4578 | GCGTGTACTACGACCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 1678 |
| Qy Dp | 1679 4638 | AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1738 |
| Qy Db | 1739 | AGATGCECACCACCACCAACGACGTGAAGCAGCTGACCAAGGCCGTGCAGAAGATCG 1798 |
| Qy | 1799 | CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1858 |
| Qy Dp | 1859 | AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT 1918 |
| Qy Dp | 1919 4878 | TCGTGAACACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGCACCCATCATCG 1978 |
| Oy Db | 1979 4938 | GCGCCGAGACCTTCTACGTGGACGCCCCCCCCAACCCCGAGACCAAGATCGGCAAGGCCG 2038 |
| Oy Db | 2039 4998 | GCTACGTGACCGACCGGGCCGGCAGAAGATCGTGACCTGACCGAGACCACCAACCA |
| Qy Db | 2099 | AGACCGAGCTGCAGCCATCCAGCTGGCCCTGCAGGACAGCGGCGAGCGA |
| Qy Db | 2159 | TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCGACAAGAGCGAGAGCG 2218 |

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PAT 20-JUN-2002
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
genetic immunization
Patent: WO 025943-A 166 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
                                      5178 AGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAGGAGGTGTACCTGGCCTGGG 5237
                                                                                                                                                                          5238 TGCCCGCCACAAGGGCATCGGCGGCAACGAGCAGGAGGAGGAGCGCCTGGTGAGCGCCGGCA 5297
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                                                                                                                                   TGCCCGCCCACAAGGGCATCGGCGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCA 2338
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                                                                                                                                                                                                                                                                      2339 TCCGCAAGGTGCTGTTCCTGGACGCCATCGATGGCGGCATCGTGATCTACCAGTA 2393
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="plasmid pVR1012x/s containing HIV genes"
a 2669 c 2519 g 1757 t
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Pred. No. 2.6e-203;
0; Mismatches 185; Indels
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AX427928
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Best Local Similarity 91.4%;
Matches 2189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artificial sequences.
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AUTHORS
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| λ G | 3441 | AGATGAGCCTGCCGGCAAGTGGAAGCCCAAGATGATCGGCGGGATCGGCGGCTTCATCA 538 | |
|----------|--------------|--|------------|
| Qy Db | 539 | AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG 598 | |
| QY | 599 3561 | IGCTGATCGGCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT 658 | |
| Qy | 659 3621 | GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCGTGAAGCTGAAGCCCGGCA 718 | 18 |
| Qy Db | 719 | TGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 778 | |
| Qy Db | 779 | CCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT 838 | |
| Qy Db | 839 | ACAACACCCCGGGGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG 898 | |
| Qy Db | 899 3861 | ACTICCGCGAGCTGAACAAGGCACCCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCC 958 | |
| Qy Db | 959 3921 | ACCCGGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT 101 | 018 980 |
| Qy Db | 1019 3981 | TCAGCGTGCCCCTGGACGACCTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 107 | 078 |
| Qy Db | 1079 | ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCA 113 | 138 |
| Oy Dp | 1139 | GCCCCAGCATCTTCCAGAGCACCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC 119 | 198 |
| Qy Db | 1199 | CCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG 125 | 258 |
| Qy | 1259 | GCCAGCACCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA 131 | 318 280 |
| Oy Db | 1319 | CCCCCGACAAGAAGCACCAGAAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC 137 | |
| Qy Db | 1379 | CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG 143 | 438 |
| Qy Db | 1439 | ACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGACAGA | 498 |
| Oy Dp | 1499 | TGCGCCAGCTGCGAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGA 155 | 558 |
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Pred. No. 2.5e-203;
); Mismatches 185;
 Location/Qualifiers
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GCGCCGAGACCTTCTACGTGCACGCCCCCCAACCGCGAGACCAAGCTGGGCAAGGCCG
                                    5793 AGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGGCCTGGG
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                       AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGGGGGGGTGAACATCG
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/db_xref="taxon:3262"/
/note="plasmid pvR1012x/s containing
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llarity 91.4%; Pred. No. 2.5e-203;
Conservative 0; Mismatches 185;
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Modifications of hiv env, gag, and pol egenetic immunization
Patent: WO 0223943-A 172 25-APR-2002;
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| 1379 CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG 1. | 1439 ACATCCAGAAGCTGGTGGCAAGCTGAACTGGGCCAGCCAG | 1499 TGCGCCAGCTGTGCAAGCTGCTGCGGGGCCCAAGGCCCTGACCGACATCGTGCCCCTGA 1 | 1559 CCGAGGAGCCGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCAG 1 | 1619 GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACT 1 | 1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1 | 1739 AGATGCGCACCGCCCACACCAACGACGTGAACGACCGAGGCCGTGCAGAAGATCG 1 | 1799 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1 | 1859 AGACCTGGGAGACCTGGTGGACCGGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGGT 1 | 1919 TCGTGAACACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG 1 | 1979 GCGCCGAGACCTTCTACGTGGACGCGCCCAACCGCGAGACCAAGATCGGCAAGGCCG 2 | 2039 GCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGA 2 | 2099 AGACCGAGCTGCAGGCCATCCAGGTGGCCGTGCAGGACAGCGCAGGTGAACATCG 2 | 2159 TGACCGACAGCCAGTACGCCCTGGCCATCATCCAGGCCCAGCCCGACAAGAGCGGGGCGGGGGGGG | 2219 AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG 2 | 2279 IGCCCGCCCACAAGGGCATCGGCGCGAACGAGCAGATCGACAALIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 2339 TCCGCAAGGTGCTGTTCCTGGACGCCATCGATGGCGCC | |
| QY Db | Qy Db | Oy Db | QY Db | Qy | QY | Qy Db | QY Db | Qy Db | QY | QY | QY | QY Dp | Qy Db | QV | Qy Db | Qy Db | ć |

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | dР | | | SUMMARIES | |
|---------------|--------|----------------|-----------------------------|----|-----------|--------------------|
| Result No. | Sco | Query Match | Query re Match Length DB | DB | ID | Description |
| 1 | 2469 | 100.0 | 2469 | 24 | ABL39959 | Synthetic construc |
| 7 | 2442.2 | | | 24 | ABL39960 | Synthetic construc |
| m | 2415.4 | | | 24 | ABL39961 | Synthetic construc |
| 4 | 2052 | | | 21 | AAA70481 | HIV FS(-) ProtMod |
| S | 2051.2 | | | 24 | ABK91616 | Modified HIV prote |
| 9 | 2042.8 | | | 24 | ABK91622 | Modified HIV prote |
| 7 | 2028.8 | | 9169 | 24 | ABK91617 | Modified HIV prote |
| 80 | 2027 | | | 24 | ABK91611 | Modified HIV prote |
| 0 | 2027 | | 12411 | 24 | ABK91613 | Modified HIV prote |

| 94 24 ABK91612 95 21 AAA70479 85 24 ABK91614 67 24 ABK91616 70 24 ABK91616 83 24 ABK91618 83 24 ABK91618 83 24 ABK91618 92 24 ABK91618 92 24 ABK91618 93 24 ABK91620 94 24 AAA70480 95 24 AAA70024 96 21 AAA70474 97 24 AABK91623 98 21 AAA93989 99 21 AAA93989 90 21 AAA70477 90 21 AAA93989 90 22 AAA48696 90 22 AAA48696 90 22 AAA48696 90 22 AAA428990 90 24 ABK39999 90 24 ABK39999 90 24 ABK39999 90 24 ABK38999 90 24 ABK38999 90 24 ABK38999 90 24 ABK38999 90 24 ABK38999 90 24 ABK38999 | 91895 91896 91897 9187 918 | Modified HIV prote HIV FS(-)_ProtMod_ Modified HIV prote Synthetic Pol Poly HIV FS(-)_ProtMod_ Synthetic Pol Poly HIV Gag-Polymerase Packaging construc HIV-1 subtype C is Nucleotide sequenc Synthetic protease Modified HIV prote HIV FS(+)_ProtInac Codon optimised HIV Modified HIV prote HIV FS(+)_ProtInac Codon optimised HIV Modified HIV prote HIV gagpol-SYNGP C HIV gagpol-SYNGP C HIV PS(+)_ProtInac Codon optimised HIV Modified HIV prote HIV gagpol-SYNGP C HIV partial leader HIV partial leader HIV partial leader HIV partial leader HIV complete leade Codon optimised Gag Synthetic RT polyn Synthetic RT polyn Synthetic RT polyn | sequence hetic RT |
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| | 90000000000000000000000000000000000000 | 80553777775882813788880001537777777881 | 000 |
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| 0255.4 0205.2 882. 20117 811. 20117 811. 20117 811. 20117 811. 20117 811. 20117 811. 19998.4 801. 9989.4 801. 9989.4 78. 91858.7 77. 91858.7 77. 91858.7 77. 91858.7 77. 91858.7 77. 91858.7 74. 8831.2 76. 8831.2 76. 6559.4 67. 6559.4 667. 6551.4 666. 6551.4 666. 6551.4 666. 6551.4 666. | 20255.4 20255.2 20107 20107 20117 20117 20117 20117 1998.4 11998.4 11998.7 11998.7 11998.7 11998.7 11998.7 11998.7 11999.7 11999.7 11991.8 11811.2 118 | 01101111111111111111111111111111111111 | 4 4 5 |

ALIGNMENTS

RESULT 1 ABL39959

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Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                         Zur Megede J, Barnett SW, Engelbrecht S, Van Rensburg EJ;
                                                                    Synthetic construct PR975(+) SEQ ID NO:30.
                                                                                                                                        Human immunodeficiency virus type C.
ABL39959 standard; DNA; 2469 BP
                                                                                                                                                                                                                        05-JUL-2001; 2001WO-US21241.
                                                                                                                                                                                                                                             05-JUL-2000; 2000US-0610313
                                                (first entry)
                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP. (UYST-) UNIV STELLENBOSCH.
                                                                                                                                                                                                                                                                                                                              WPI; 2002-154920/20.
                                                                                                                                                                       WO200204493-A2.
                                               15-MAY-2002
                                                                                                                                                                                                17-JAN-2002.
                                                                                                                                                    Synthetic.
                        ABL39959;
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New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy

Claim 1; Fig 8; 233pp; English.

The present invention describes expression cassettes comprising a polynouleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynocleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABEL40054 and ABB06225 represent sequences used in the exemplification of the present invention.

Sequence 2469 BP; 571 A; 833 C; 761 G; 304 T; 0 other;

Query Match 100.0%; Score 2469; DB 24; Length 2469; Best Local Similarity 100.0%; Pred. No. 8.2e-301; Matches 2469; Conservative 0; Mismatches 0; Indels 0; Gaps

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Db 541 GTGCGCCAGTACGACCAGATCCTGATCGAGGACGAAGAAGACCATCGGCACCGTG 600
Oy 601 CTGATCGGCCCACCACCCGTGAACATCATCGCCGCAACATGACCTGACCTGGGCTGC 660

DD 601 CTGATCGGCCCCACCCCGTGAACATCGTCGCCGCAACATGCTGACCTGGCCTGC OY 661 ACCTGAACTTCCCCATCAGCCCCATGAGCCGTGAAGCTGAAGCCGGCATG

721 GACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC 78

1080 1200 1260 1500 1620 1680 1800 1020 1080 1200 1320 1560 1620 ATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAG 1860 900 960 781 ATCTGCGAGGAGATGGAGAAAGGAGGCCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC 841 AACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGAC TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTC 1021 AGGGTGCCCCTGGACGAGGACTTCCGCAAGTACACGCCTTCACCATCCCCAGCATCAAC AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC CCCGACAAGAAGCACCACAAAGGAAGCCCCCTTCCTGTGGATGGGCTACGAGCAGCTGCACCC GACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACGAC ATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTG GTGTACTACGACCCCAGCAAGGACCTGGTGGCCCAGATCCAGAAGCAGGGCCACGACCAG ATGCGCACCGCCCACACCAACCACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCC ATCTGCGAGGAGATGGAGAAGGAGGCCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC AACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGAC GAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGC CAGCACCGCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGTGGGGGCTTCACCACC CCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCC CGCCAGCTGTGCAAGCTGCTGCGGGGGGGCGCAAGGCCCTGACCGACATCGTGCCCTGACC TGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG 1081 1081 1441 1201 1261 1261 1321 1321 1381 1381 1501 1501 1621 1681 1681 1741 721 781 901 901 196 1561 1621 1561 1801 a g 셤 g g οg δ QΥ g δy Db g q qq g g g g à Ω δ δ Qγ οy οy Qγ ò Q ò Q q ò q Ω

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type C; antigenic HIV type C protein; ag; pol; vif; vpr; tat; rev; vpu; env; nef;
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                                 GTGAACACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGC
                                                                                                                     GCCGAGACCTTCTACGTGGACGCCCCCCCAACGCGAGACCAAGATCGGCAAGGCCGGC
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immunogenic; immunisation; gag; pol; vif
immunostimulant; gene therapy; gene; ds.
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The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06215 represent sequences used in the exemplification of the present invention.
                                                                                        New polynucleotides encoding antigenic HIV Type C polypeptides, usefulin applications including DNA immunization or generation of packaging
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99.6%; Pred. No. 1.9e-297;
tive 0; Mismatches 3;
                                 Engelbrecht S,
                                                                                                                     cell lines, particularly in gene therapy
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                               Barnett SW,
(UYST-) UNIV STELLENBOSCH
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                                                            WPI; 2002-154920/20.
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| ACCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAGCTGAAGCTGAAGCCCGGCATG | GACGCCCCAAGGTGAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCTTIIIIIIIIII | ATCTGCGAGGAGATGGAGAGAGGGAAGATCACCAACATCGGCCCCGAGAACCCCTAC | AACACCCCGTGTTCGCCATCAAGAAGAAGACACCACCAAGTGGGGCAAGCTGGTGGCCCCCTTTTTTTT | TTCCGCGAGCTGAACAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC | CCCGCCGGCCTGAAGAAGAAGAAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTC | AGGTGCCCTGGAGGACTTCCGCAAGTACACGCCTTCACCATCCCCAGCATCAAC | AACGAGACCCCGGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCCAGC | CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCTIIIIIIIIII | GAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGC | CAGCACCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCTGCGGTGGGGCTTCACCACC | CCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCTTTCTTGTTTTTTTT | GACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACGAC | ATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTG | CGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACC | GAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCCGCGCCGCGCCGTGCACGCCGGAGCCCGTGCACGCCGAGACCGCGAGACCTGCCGCGAGCCCGAGGCCGGCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCACGCCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCACGCCCCACGCCCACGCCCACGCCCACGCCCACGCACACCCCCACGCCCACACACCCCCACGCCCACACACCCCCACACACCCCCACACACCCCCACACACA | GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACAGGIIIIIIIIII | TGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG |
| 661 | 721 | 781 | 841 | 901 | 961 | 1021 | 1081 | 1141 | 1201 | 1261 | 1321 | 1381 | 1441 | 1501 | 1561 | 1621 | 1681 |
| Qy Db | Qy | Qy | Oy Dp | Qy | Qy | Qy Db | Oy Dp | Oy Dp | Q _Y | Qy | Qy Dp | Oy Dp | Qy Db | Qy | Qy | Qy | Oy Dp |

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                                                 1801 AIGGAGAGCAICGIGAICIGGGGCAAGACCCCCAAGIICCGCCIGCCCAICCAGAAGGAG
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nef;

Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; immunostimulant; gene therapy; gene; ds.

Human immunodeficiency virus type C. Synthetic.

WO200204493-A2

17-JAN-2002.

Synthetic construct PR975YMWM SEQ ID NO:32.

(first entry)

15-MAY-2002

ABL39961;

BP.

ABL39961 standard; DNA; 2457

2001WO-US21241 05-JUL-2000; 2000US-0610313 05-JUL-2001;

UYST-) UNIV STELLENBOSCH CHIR) CHIRON CORP

EJ; Rensburg Van Ś Engelbrecht SW, Zur Megede J, Barnett WPI; 2002-154920/20.

usefu] pe C polypeptides, usefu generation of packaging New polynucleotides encoding antigenic HIV Type C in applications including DNA immunization or gene cell lines, particularly in gene therapy

Claim 1; Fig 10; 233pp; English.

The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gay Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (1). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL30942 to ABL40054 and ABB06215 represent sequences used in the exemplification of the present invention.

Sequence 2457 BP; 566 A; 837 C; 754 G; 300 T; 0 other;

420 120 180 300 300 360 360 420 480 541 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACGTG 600 Gaps 9 9 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGCGCCACCAACATCCTGATGCAG AGCCGCGAGCTGCAGCTGCGCGCGCAACCCCCGCAGCGAGGGCGGCGCCGAGGCCCAG 1 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCCAACATGCTGAGCAG GGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCC TTCCCCCCAGGGCAAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACC CGCAGCAACTICAAGGGCCCCCAAGCGCATCAACTGCTTCAACTGCGGCAAGGAGGGC CACATCGCCCGCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAG AGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCAGCGAGGCCGGCGGCGAGCGCCAG GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCCCCCCTGGTGAGCATCAAGGTG GGCGGCCAGATCAAGGAGGCCCTGCACACCGGCGCCCGACGACGACCGTGCTGGAGGAG ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGCATCGGCGGCGTTCATCAAG DB 24; Length 2457; 12; 6; Indels Score 2415.4; DB 2 Pred. No. 4.2e-294; 0; Mismatches 6; Query Match
Best Local Similarity 99.3%;
Matches 2451; Conservative (Г 121 181 61 121 181 61 301 301 361 361 421 121 481 481 δy П ò QQ ò g δy qq qq qq Qγ δ g ò δy Оp δλ g ò

1020 1201 GAGATCGTGATCTACCA-----GGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGC 1254 1320 1428 CCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCC 1380 ATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTG 1500 960 720 720 780 900 1081 AACGAGACCCCCGGCATCCGCTACCAGTACATGCTGCCCCAGGGCTGGAAGGCCAGC ACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGGCATCCCCCAC CCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCACGTGGGCGACGCCTACTTC AGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC CTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGC GACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC AACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGAC 1021 AGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAC AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC GACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACGAC ATCTGCGAGGAGATGGAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGGGGCCCGCAACCCC GAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGC CAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTTCAGCACC CGCCAGCTGTGCAAGCTGCTGCGCGCGCCCAAGGCCCTGACCGACATCGTGCCCTGACC CGCCAGCTGTGCAAGCTGCTGCGGGGGCGCAAGGCCCTGACCGACATCGTGCCCCTGACC GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACAG CCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCAT----CGAGCTGCACCC GAGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGGCCCGTGCACGGC 781 841 1141 601 601 199 721 721 901 901 196 961 1021 1141 1201 1261 1255 1321 1381 1441 1549 1081 1315 1369 1429 1501 1489 1561 1621 δ q g Q g Оp Öζ ó ŏ δ ò ö g ŏ g ΟŻ qq Qγ q δý q δ g qq g Оp ò ŏ δ δ ó QQ

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                          1681 TGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG 1740
                                                                                                1789 ATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAG 1848
1609 GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAG 1668
                                                                                  ATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCC 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1; AIDS; Gag-reverse transcriptase; vaccine; expression cassette;
                                       1669 TGGACCTACCAGGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG
                                                                                                                                                                                                              2389 GACCTGTACGTGGGCGCGCGCGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCAC
                                                                                                                                        ATGGAGGATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAG
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                                                                                                                                                                                                                                                      1921 GTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGC
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The present sequence is the coding sequence of a synthetic HIV Gag reverse transcriptase expression cassette, FS(-) ProtWod_RTopt(+). The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGGACCTGCCTTCCTGCAGGCAAGGCCCGCGAGTTCAGCAGCGAGCAGCAGCCGCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                   Ξ
                                                                                                                                                                                                                                                              Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                    Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGCC ----ACAACCCCCCCAGCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.1%; Score 2052; DB 21; Length 2312; llarity 93.6%; Pred. No. 1.1e-248; Conservative 0; Mismatches 135; Indels 12;
                                                                                                                                                                                   Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2312 BP; 533 A; 750 C; 732 G; 297 T; 0 other;
                                                                                                                                                                                    Lian Y,
                                                                                                                                                                                   Srivastava I,
C;
                                                                                                                                                                                                                                                                                                                               Claim 7; Fig 75; 391pp; English.
                                                                          99WO-US31245
                                                                                                       98US-0114495
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                                                                                                                                                                                    Zur Megede J,
alby M, Walker
                                                                                                                                                                                                                                    WPI; 2000-452400/39.
                                                                                                                                                     (CHIR ) CHIRON CORP.
                                                                                                                                                                                                     Selby M,
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             WO200039302-A2
                                                                                                         31-DEC-1998;
                                                                                                                        01-DEC-1999;
                                                                        30-DEC-1999;
                                          06-JUL-2000
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Matches 2165;
                                                                                                                                                                                      Barnett S,
                                                                                                                                                                                                     Greer C,
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|---|---|---------------------|---|--|--|------------------------------|---|
| ACCTGCTGACCCAGATGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACGGT CCGTGAAGCTGAAGCAGGCCCCAAGGTGAAGCAGTGCCCCTGACCGA [| | | B AGCCTTCCGGCCCCCCACCCGAGATCTACCATACCATAC | TGCTGCGCTGGGGCTTCACCACCCCGACAAGAACACCAGAAAGGAGCCCCCTTCCTGT | B AGGAGGCTGGACCGTGAACCACATCCAGAAGCTGGCGCAAGCTGGACCGAACCCAGCC | | TCCAGAAGCAGGCCACGACCAGTGCACCTACCAGATCTACCAGGAGCCCTTCAAGAACC |
| 481 698 541 758 601 818 818 878 | 727 938 78 9 38 8 4 3 8 4 | 1058 901 1118 | 1178 1021 1238 1081 | 1296 1141 1358 1201 | 1418 1261 1478 1321 | 1538 1381 1598 1441 | 1658 1501 1718 1561 |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | DP OX | Oy Oy Db | Oy Oy Ob | oy Oy Dp | Oy Oy Ob | 0y 0y 0b | Oy Oy Dp |

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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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                                               CCGAGGCCGTGCAGAAGATCGCCATGGAGGATCGTGATCTGGGGCAAGACCCCCAAGT
                                                                                                CCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGC
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                                                                                                                                                 1958 TGGAGAAGGAGCCCATCATCGGCGCCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCG
                                                                                                                                                                                                 AGACCAAGATCGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGATCGTGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified HIV protein-encoding plasmid DNA #168.
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                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2961 TGGCCGAGGCCATGAGCAAGGTGAACAACACCAACATGATGATGCAGCGCAGCAACTGCA 3020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 AGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCA 133
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                                                                                                                                                                                                                     New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9166 BP; 2227 A; 2662 C; 2513 G; 1764 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163; Indels
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Pred. No. 1.2e-248;
0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 766-769; 794pp; English.
                                                              US DEPT HEALTH & HUMAN SERVICES. CHADRABARTI B K.
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92.6%;
14-NOV-2000; 2000US-252115P
                    28-MAR-2001; 2001US-279257P
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                                                                                                                                                                           WPI; 2002-452382/48
                                                                                                                                  Nabel GJ, Huang Y;
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3500 TGGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCACAAGGCCATCGGCACCGTGC 3559
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                                                                                                                                                                            CCCTGAACTTCCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG
                                                                                                                                                                                                                                                                                           722 ACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                              782 TCTGCGAGGAGATGGAGAAGGAGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACA
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                                                         602 TGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCA
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CTL.
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                                                                                             1802 TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA 1861
           4640 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCGCAA
                                                            GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGA
                                                                                                                                                            TGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGC
                                                                                                                      4760 CCGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCAAGCTGCCCATCCAGAAGGAGA
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                                                                                                                                                                                                                                              CCGAGACCTTCTACGTGGACGCGCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCT
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ARK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3314
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                                                                                                                                                                                                                                                                                                                                        invention relates to a nucleic acid molecule encoding a modified
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                                                                                                                                                                                             New modified human immunodeficiency virus Env, Gag, Pol of Nef its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
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0; Mismatches 177;
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                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES
14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
                                                                            CHADRABARTI B
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| Dp | 3495 | IGGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCACAAGGCCATCGGCACCGTGC 3554 | |
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| Oy Db | 602 3555 | TGATGGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCA 661 | |
| ro d | 99 | ~1 | |
| Q C | - | cctbaacticcccaicagccccaicgagaccgigcccgigaagcigaagcccggcaigg 36 | |
| Qy Dp | 722 3675 | ACGCCCCAAGGTGAACCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCA 781 | |
| Oy Dp | 782 | TCTGCGAGGAGATGGAGAGGCAAGATCACCAAGATCGGCCCGAGAACCCCTACA 841 | |
| οy | 842 | CACCCCGGGTTTCGCCATCAAGAAGAAGACAGCACAAGTGGGGCAAGTGGTGGTGGACT 90 | |
| Db | 3795 | ACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGC | |
| Qy Db | 902 | TCCGCGAGCTGAACAAGCGCACCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACC 961 | |
| QQ Dp | 962 3915 | CCGCCGCCTGAAGAAGAAGAAGAGCGTGACCGTGGACGTGGGCGACGCTACTICA 1021 | |
| Qy Dp | 1022 | GTACACCGCCTTCACCATCCCCAGGATCAACA 10 | |
| οy | 08 | SACCCCGGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCC 114: | |
| QQ | 03 | CGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGO | |
| Qy Dp | 1142 | CCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCGCAACCCCG 1201 | |
| Qy Db | 1202 | AGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGCC 1261 | |
| Qy Db | 1262 | | |
| Qy Db | 1322 | SATGGGCTACGAGCTGCACCCCG 13 | |
| Qy Db | 1382 | SAAGGAGAGCTGGACCGTGAACGACA 144. | |
| ò | 44 | AGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATTACCCCGGCATCAAGGTGC 150 | |
| . a | 39 | | |
| Oy Db | 1502 4455 | | |
| Qy Dp | 1562 | | |
| 6 A | 62 | GTACTACGACCCCAGCAAGGACCTGGTGGCCAGATCCAGAAGCAGGGCCACGACAGT 168° GTACTACGACCCCAGCAAGGACCTGGTGGCCAGATCCAGAAGCAGGCCACGACCAGT 168° GTACTACGACCAGCAAGGACGTGTGTGTGTGTGTGTGTGT | |

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                                           4695 TGAAGGGCCCCACACCACCACCACGAGGTGAAGCAGCTGACGAGGCCGTGCAGAAGATGGCCA 4754
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1682 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGA 1741
                                                                   1802 TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA 1861
                                                                                                                                                                                                                                                                                                                                              4635 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGAACCGGCAAGTACGCCGCAA
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                                 1742 TGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA
                                                                                                             1922 TGAACACCCCCCCCCGGGGAACTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG
                                                                                                                                                       1982 CCGAGACCTICTACGTGGACGCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCT
                                                                                                                                                                                                                                                                            2342 GCAAGGTGCTGTTCCTGGACGCCATCGATGCCGCCATCGTGATCTACCAGTA 2393
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.

14-AUG-2000; 2000US-225097P. 14-AUG-2001; 2001WO-US25721.

WO200232943-A2.

Synthetic

25-APR-2002

protein-encoding plasmid DNA #169.

Modified HIV

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DEPT HEALTH & HUMAN
14-NOV-2000; 2000US-252115P. 28-MAR-2001; 2001US-279257P.
               CHADRABARTI B K.
                               WPI; 2002-452382/48.
                       Nabel GJ, Huang Y;
            SO (HSSO)
                (CHAD/)
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SERVICES

DNA and New modified human immunodeficiency virus Env, Gag, Pol of Nef its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection

Disclosure; Page 769-772; 794pp; English.

The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cyttoxic Tiymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK01449.ABK01449.ABK01449.ABK01449.ABK01449.ABK01440.ABK01460.ABK0144

Sequence 9169 BP; 2227 A; 2668 C; 2505 G; 1769 T; 0 other;

AGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGCTTC 3262 AGGTTTGGGGAAGAGACAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAACTG 3322 AGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGGCAAGGGGCCACATCGCCCGCA 133 ACTGCCGCGCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGATGA 193 AGGACTGCACCGAGGCCAACTTCTTCGCGAGGACCTGGCCTTCCCCCAGGGCA 253 481 16; Gaps TGGCCGAGGCCATGAGCCAGGCCACCAGGGCCAACATGCTGATGCAGCGCAGCAACTTCA 73 AGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTGC GCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCCGACGACGACGTGCTGGAGGAGA ---CCCTGAACTICCCCCAGAICACCCTGTGGCAGCGCCCCCTGGTGAGCAICAAGGTGG Query Match 82.2%; Score 2028.8; DB 24; Length 9169; Best Local Similarity 91.7%; Pred. No. 7.5e-246; Matches 2194; Conservative 0; Mismatches 182; Indels 16; 14 2967 3027 3084 3144 3263 3383 74 194 3203 134 254 365 422 QQ pp QYò δy g δ οg Ω g qq QY ŏ qq δ q

TGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATCGGCGGCGCATCGGCGGCGTTCATCAAGG

ò a TGGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGGCAAGAAGGCCATCGGCACCGTGC

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3742 3922 3503 TGGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCACAAAGGCCATCGGCACCGTGC 3562 4342 AGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCG 1621 4642 901 781 ACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT 1082 ACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCC 4043 ACGAGACCCCGGCAICCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCC CCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCGCCGCAACCCCG AGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGCC 1262 AGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACCC GCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCG TGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCCAGCTGGGCTGCCA 662 CCCTGAACTICCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG 722 ACGCCCCAAGGIGAAGCAGIGGCCCCIGACCGAGGAGAAGAICAAGGCCCIGACCCCA TCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACA 3803 ACACCCCCGTGTTCGCCATCAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACC CCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTCA 1022 GCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGGCCTTCACCATCCAGCATCAACA 4223 AGCACCGCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGCGCGTGGGGCTTCACCACCC 1322 CCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCG TCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGC 1382 ACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACGACA TGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGT AGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGCCCGTGCACGGCC 602 842 782 1142 1202 962 4343 1442 4403 1502 1562 4283 4463 q δy В δ g δy qq ò δy g Οy qq ŏ g QΥ Op qq ŏ δλ ŏ qq δŏ qq δ g δŻ g q g ò ŏ ŏ q δy

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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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                                                                                                                                                                                                                                                                                               4883 TGAACACCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG 4942
                                                                                                                                                                                                                                                                                                                                                                                                                    1682 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGA 1741
                                                                                                                                1802 TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA 1861
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                                                                                                                                                                                                                 4823 CCTGGGAGGCCTGGTGGACCGAGTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG
                                                                                                                                                                                                                                                                                                                                CCGAGACCTTCTACGTGGACGCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCT
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                 4643 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGAGCCGGCAAGTACGCCCGCA
                                                                                               4703 TGAAGGGCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA
                                                                                                                                                   1862 CCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG
                                                                                                                                                                                                                                                                  TGAACACCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCCATCATCGGCG
                                                                 1742 TGCGCACCGCCCACACCACCACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytocoxic Tymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or
                                                                                                                                                                                                                                                                                                                                                                                                    AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
                                                                                                                                                                                                                                                                 invention relates to a nucleic acid molecule encoding a modified HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.1%; Score 2027; DB 24; Length 9194; 91.6%; Pred. No. 1.3e-245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9194 BP; 2232 A; 2671 C; 2524 G; 1767 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                  Disclosure; Page 750-753; 794pp; English.
                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES. (CHAD/) CHADRABARTI B K.
14-NOV-2000; 2000US-252115P.
                28-MAR-2001; 2001US-279257P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 2194; Conservative
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| GGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCACAAGGCCATCGGCAC | | 659 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCGTGAAGCTGAAGCCGGGCA | 719 TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG | 779 CCATCTGCGAGGAGATGGAGAGGGGGAAGATCACCAAGATCGGCCCCGAGAACCCCT | 839 ACAACACCCCGTGTTCGCCATCAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG | 899 ACTTCCGCGAGCTGAACAAGCGCACCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC | 959 ACCCGCCGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT | 1019 TCAGCGTGCCCCTGGACGACGACGACTTCCGCAAGTACACCGCCTTCACCATCCCCGGCGTCACAGCATCACAGCATCCCCAGCATCACAGGACTTCCGCAAGACTTCCGCAAGACTTCCGCAAGACATCCCCAAGACATCCAAGAACATCACCAAGAACATCACAAGAACATCAAGAACATCAACAAGAACATCAAGAACATCAAGAACATCAAGAACATCAAGAACATCAAGAACATCAAGAACAACAACAACAACAACAACAACAACAACAACAAC | 1079 ACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA | 1139 GCCCCAGGATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC | 1199 CCGAGATCTGATCTACCACTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG | 1259 GCCAGCACCGCGCCAAGATCGAGGAGCTGGGCAAGCACCTGCTGCTGCGGTGGGGCTTCACCA | 1319 CCCCGGACAAGAAGCACCAGAAGCAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC | 1379 CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACG | 1439 ACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGACTGTACCCGGGCATCAAGG | 1499 TECGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCTGA | 1559 CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGGAGCCCGTGCAGGCAG | 1619 GCGTGTACTACGACCCCAGCAAGGACCTGGCCGAGATCCAGAAGCAGGGCCACGACC |
| Db Qy | qq | Qy Db | Qy Db | Qy | Qy Dp | QY | QY | Qy Db | Qy Db | Qy Db | Qy Db | Qy Db | Qy | Qy Dp | Qy Db | Qy Db | Qy Db | Qy |

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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1738
           GCTACGTGACCGACCGGCGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGA 2098
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                                         1919 TCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCCATCATCG
                                                                                                                                                                                 1799 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGG
                                                                                                                                                                                                                GCGCCGAGACCTTCTACGTGGACGCCCCCGCCAACCGCGAGACCAAGATCGGCAAGGCCG
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these are useful for ameniorating the symptoms of adduired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T Lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Brv, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular
                                                                                                                                                                                                                New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 756-760; 794pp; English.
                                                               US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid DNA sequences of the invention.
14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
                                                                                      CHADRABARTI B K.
                                                                                                                                                                       WPI; 2002-452382/48
                                                                                                                                 Nabel GJ, Huang Y;
                                                                 (USSH)
                                                                                      CHAD/)
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Sequence 12411 BP; 2938 A; 3733 C; 3476 G; 2264 T; 0 other; Indels Score 2027; DB 24; Pred. No. 1.2e-245; 0; Mismatches 185; 82.1%; 91.6%; Conservative Similarity

4, TGGCCGAGGCCATGAGCCAGGTGACCAACAGCGCCCACCATCATGATGCAGCGCGGCAACT 3026 TGAAGGACTGCACCGACGCGACAGGCTAA-TTTTTAGGGAAGATCTGGCCTTCCCACAAG 3205 GGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGC 3265 3266 TTCAGGTTTGGGGAAGAGACAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAA 3325 419 TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGG 478 -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGG 418 71 TCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCCAAGGAGGCCCACATCGCCC 130 GCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGCCCACCAGA 190 TGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG 250 GCAAGGCCCGCGAGGTTCCCCCAGCGAGCAGAACCGCGCCAACAGCCCCCACCAGCCGCGAGC 310 TGCAGGTGCGCGG-----CGACAACCCCCGCAGGCGGGCGGCGGCGGCGCCAGGGCA 364 16; Gaps TGGCCGAGGCCATGAGCCAGG --- CCACCAGCGCCAACATCCTGATGCAGCGCAGCAACT 70 TAGGGGGCCAGCTGAAGGAGGCCCTTCTAGACACCGGCGCGCGACGACACCGTGCTGGAGG AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGATCGGCGGCGTTCATCA Best Local Sim Matches 2194; Query Match 479 131 3087 3147 3386 3446 2967 3206 14 191 251 311 qq g Q Д Óλ δ qq g g q ò q οy ŏ ŏ ò ò ð

AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG

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4645 1558 1438 3865 4046 ACAACGAGCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCA 4105 GCCAGCACCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA 1318 3745 TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 1078 TCAGCGTGCCCCTGGACAAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 4045 1079 ACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA 1138 GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCCGCAACC 1198 3566 TGCTGGTGGGCCCCACCCCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGATCGGCT 3625 3506 AGGIGGGCCAGTACGACCAGATCCIGATCGAGATCIGCGGCCACAAGGCCATCGGCACCG 3565 778 CCGACATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG 4286 CCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACG 4466 TGCGCCAGCTGTGCAAGCTGCTGCGCGGCACCACAAGGCCCTGACCGAGGTGGTGCCCCTGA 1559 CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG 4526 CCGAGGAGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGCCGTGCACG 1619 GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 4586 GCGTGTACTACGACCCCAGCAAGGACCTGATCGCCGAGATCCAGAAGCAGGGCCAGGCC 1199 CCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC 1499 TGCGCCAGCTGTGCAAGCTGCTGCGGGGGGCGCCAAGGCCCTGACCGACATCGTGCCCTGA 3746 AGATCTGCACCGAGATGGAGAAGGAGGCCAAGATCAGCAAGATCGGCCCCGAGAACCCCT 3926 ACCCCCCCCCCCGCCTGAAGCAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 3686 TGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGGTGG ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGCGGACGTACT 599 TECTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCAGCTGGCCT 659 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA 779 CCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT 839 ACAACACCCCGGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG ACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC 4106 1379 719 668 959 1019 3986 1139 4166 1259 4226 1319 Dp Dp QQ QQ q δ a δλ q δ Q g QΥ g ŏ δy qq δ qq Qγ ŏ δ δ Dp q δλ g δ Óλ ÓΥ g δ Q δ

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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation. AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CTL.
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                 1799 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1858
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1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA
                                                                                                                                                                                AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGGAGTGGGAGT
                                                                                                                                                                                                                                                                                                     GCGCCGAGACCTTCTACGTGGACGGCGCCGAACCGCGAGACCAAGATCGGCAAGGCCG
                                                           1739 AGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
                                                                                                                                                 CCACCGAGGGATCGTGATCTGGGGCAAGACCCCCAAGTTCAAGCTGCCCATCCAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2339 TCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTA 2393
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these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Brv, day, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2967 TGGCCGAGGCCATGAGCCAGGTGACCAACAGCGCCACCATCATGATGCAGCGCGGCAACT 3026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24; Length 9194;
                                                                                                                                                                       New modified human immunodeficiency virus Env, Gag, Pol of Nef its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9194 BP; 2232 A; 2672 C; 2523 G; 1767 T; 0 other;
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Pred. No. 2e-245;
0; Mismatches 186; Indels
                                                                                                                                                                                                                                                             Disclosure; Page 753-756; 794pp; English.
                                                  HEALTH & HUMAN SERVICES.
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91.6%;
2000US-252115P.
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14-NOV-2000;
28-MAR-2001;
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Matches 2193;
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| AGGTGGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCACAAGGCCATCGGCACCG | TGCTGATCGGCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT | GCACCCTGAACTTCCCCATCAGCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA | TGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG | CCATCTGCGAGGAGGAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCT | ACAACACCCCGGGTGTTCGCCATCAAGAAGGACAGCACCAAGTGGGGGAAGCTGGTGG | ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC | ACCCGCCGGCCTGAAGAAGAAGAGGGGGCGGCCGTGCTGGACGTGGGCGACGCCTACT | TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCGGCATCA | ACAACGAGACCCCCGGCATCCGCTACCAGTACGAGGTGCTGCCCCGGGGCTGGAAGGGCAGCA | GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGGGCCCGCAACC | CCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGGTCG | GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA | CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCACCTILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGGGAAGGAGGGCTGGACCGTGAACG | ACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCA | TGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCCAAGGCCCTGACCGACC | CCGAGGAGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGGAGCCGTGCACGCCGTGATTCTTTTTTTT | GCGTGTACTACGACCCCAGCAACCTGGTGGCCGAGATCCAGAAGCAGGCCACGACC |
| 3506 | 599 3566 | 659 3626 | 719 | 3746 | 3806 | 3866 | 959 3926 | 1019 3986 | 1079 | 1139 | 1199 | 1259 | 1319 | 1379 | 1439 | 1499 | 1559 4526 | 1619 |
| qq | Qý | Qy Dp | Qy Dp | Qy Db | QY | Qy Dp | Qy | Qy Dp | QY | Qy Db | Oy Dp | Qy Db | Ογ Db | QY | Qy Db | Qy Db | Oy Db | oy Db |

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HIV-1; AIDS; Gag-reverse transcriptase; vaccine; expression cassette; ss.
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1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGCAAGTACGCCA 1738
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               4646 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGGCAAGTACGCCC
                                                                    1799 CCATGGAGGGATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG
                                                                                                                         1859 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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                                                     1739 AGATGCGCACCGCCCACACCACCACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
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3;
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The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
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82.0%; Score 2025.2; DB 21; Length 2306;
Best Local Similarity 93.3%; Pred. No. 2.6e-245;
Matches 2156; Conservative 0; Mismatches 138; Indels 18;
                                                                                                                                                                                                           present sequence is the coding sequence of a synthetic HIV
                                                                                                                                Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CTL.
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New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection -

Disclosure; Page 739-741; 794pp; English.

The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.

Sequence 9189 BP; 2232 A; 2671 C; 2524 G; 1762 T; 0 other;

4; 3146 3260 3320 3380 3440 2967 TGGCCGAGGCCATGAGCCAGTGACCAACAGCGCCACCATCATGATGCAGCGGCGACT 3026 3560 190 310 71 TCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130 418 478 538 598 70 TCCGCAACCAGCGCAAGATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACACCGCCC GCAACTGCCGCCCCCCCCCGCAAGAAGGCCTGCAAGTGCGGCAAGGAGGGCCACCAGA TGAAGGACTGCACCGAGCGCCAAGCCTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG GGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAAACAGCCCCACAGAAGAGAGC TGCAGGTGCGCGG-----CGACAACCCCCGCAGGGAGGCCGGCGGCGAGGCCAAGGGCA TTCAGGTTTGGGGAAGAGACAACACTCCCTCAGAAGCAGGAGCCGATAGACAAGGAA AGGTGCGCCAGTACGACCAGATCCTGATCGAGGATCTGCGGCAAGAAGGCCATCGGCACCG AGGTGGCCCAGTACGACCAGATCCTGATCTGCGGCCACAGGCCATCGGCACCG GCAAGGCCCGCGGGGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCGCGGAGC -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGG TGGCCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGG AGATGAGCCTGCCCGCCAAGTGGAAGCCCAAGATGATCGGCGGCGATCGGCGGCTTCATCA TGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT TGCTGGTGGGCCCCCACCCCCGTGAACATCGGCCGCAACCTGCTGACCCAGATCGGCT DB 24; Length 9189; 0; Mismatches 184; Indels Pred. No. 1.4e-244; 81.8%; Score 2018.6; 91.48; Best Local Similarity 91.4 Matches 2190; Conservative Query Match 3027 131 3087 3147 3201 311 3261 365 419 3501 3561 251 539 599 191 g δ pp g qq qq g ð ò ò à Ω q Op 임 ò οy oy οy ò ò

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GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCGGTGAAGCTGAAGCCCGGCA

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3860 1018 1078 4640 4100 4400 1498 4460 1678 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1738 1739 AGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACGAGGCCGTGCAGAAGATCG 1798 GCCAGCACCGCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGGCTTCACCA TGGACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 3681 TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGGTGG 3741 AGATCTGCACCGAGATGGAGAAGGAGGGCAAGATCAGCAAGATCGGCCCCGAGAACCCCT 899 ACTICCGCGGAGCTGAACAAGCGCACCCAGGACTTCTGGGGAGGTGCAGCTGGGCATCCCCC 959 ACCCCGCCGCCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGCGGCCCTACT 1019 TCAGCGTGCCCCTGGACGAGTTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 1079 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC CCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG 4161 CCGACATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG CCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACG 839 ACAACACCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG 4041 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA GCCCCGCCATCTTCCAGTGCAGCATGACCAAGATCCTGGAGCCCTTCCGCAAGCAGAACC GCCAGCACCGCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGCGCGTGGGGCTTCACCA CCCCCGACAAGAAGCACCAGCAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC TGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCCAAGGCCCTGACCATCGTGCCCCTGA CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGCAGCCCGTGCACG CCATCTGCGAGGAGATGGAGAAGGAGGCCAAGATCACCAAGATCGGCCCCGAGAACCCCT 4461 TGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGAGGTGGTGCCCCTGA GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC AGTIGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCC 4101 1319 1139 1259 4221 4281 1379 1439 1499 1559 1619 1679 1199 4521 4701 q Db δλ qq Db 셤 qq ŏ q 원 g q QQ QQ Qγ QΥ Ω δ ò Qδ Qy δ g δλ qq Q qq δ q Ω g δ qq

Tue Feb

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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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                                                                                                     TCGTGAACACCCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG 1978
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                                                                 GCGCCGAGACCTTCTACGTGGACGGCGCCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
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                                                    AGACCTGGGAGACCTGGTGGACCGACTAČTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified HIV protein-encoding plasmid DNA #171.
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nabel GJ, Huang Y;
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
                                                                                                                                                             The invention relates to a nucleic acid molecule encoding a modified HIV
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                 Pol of Nef
or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9167;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9167 BP; 2225 A; 2668 C; 2517 G; 1757 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 185; Indels
                 New modified human immunodeficiency virus Env, Gag, Pol
its encoded protein, useful as vaccines for genetic or
immunisation for acquired immunodeficiency syndrome or
immunodeficency virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.7%; Score 2017; DB 24; 91.4%; Pred. No. 2.3e-244;
                                                                                                                     Disclosure; Page 775-778; 794pp; English.
                                                                                                                                                                                                                                                                                                                                                                    plasmid DNA sequences of the invention.
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Matches 2189; Conservative
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CCATCTGCGAGGAGGAAGGAGGGCAAGATCACCAAGATCGCCCCGAGAACCCCT
                                                             3738 AGATCTGCACCGAGATGGAGAAGGAGGCCAAGATCAGCAAGATCGGCCCCGAGAACCCCT
                                                                                    ACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG
                                                                                                                                        3858 ACTICCGCGAGCTGAAAGCGCACCCAGGACTICTGGGAGGTGCAGCTGGGATCCCCC
                                                                                                                                                                     ACCCGCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGGACGTGGGCGACGCCTACT
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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New modified human immunodeficiency virus Env, Gag, Pol of Nef I its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection

and

DNA

Disclosure; Page 760-763; 794pp; English.

The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gay, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gay, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.

Sequence 9170 BP; 2225 A; 2669 C; 2519 G; 1757 T; 0 other;

3440 3621 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCGGGCA 3680 310 478 718 TCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130 TCCGCAACCAGCGCAAGATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACACCGCCC CTGTATCCTTTAGCTTCCCTCAGATCACTCTTTGGCAGCGACCCCTCGTCACAATAAAGA GCAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGA TGAAGGACTGCACCGAGCCCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG GCAAGGCCCGCGAGTTCCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGC TGCAGGTGCGCGG-----CGACAACCCCCGCAGCGAGGCCGCCGAGCGCCAAGGGCA -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGG TGGCCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGG TGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCCAGCTGGGCT AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCCATCGGCACCG GCACCCTGAACTTCCCCCATCAGCCCCATCGAGACCGTGCAGGTGAAGCCCGGGCA 21; Length 9170; Indels DB 24; Score 2017; DB 24; Pred. No. 2.3e-244; 0; Mismatches 185; . 0 81.7%; ilarity 91.4%; Conservative 0 Similarity Matches 2189; Match Local S 2967 71 3027 131 3087 3147 3201 3261 3321 479 3441 14 251 311 539 3501 3561 191 365 419 Query δ Db δy g Qγ Db δy g οy QQ δy Q Ω qq ŏ QQ δy 엄 ò Q ò g ŏ

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rockefeller.0.1211 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to adenosylhomocysteinase (EC 3.3.1.1), mRNA sequence.

DEFINITION

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/note="syn: Phreatamoeba balamuthi"
321 c 303 q 139 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2274 CTGGGTGCCCCCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAA 2333
                                                                                                                                                   Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 CATCGCGCAGGCCGCGTCTCGGTCTTCGCCTGGAAGGGCGAGAACCTCCAGGAGTACTG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 GAGTGCACCTGGAAGGCCCTGTGCTTCGGCCCCTACCAGGGCCCTCAGATCATCGTCGA 398
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Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
21819461
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Pred. No. 9.9e-05;
0; Mismatches 376; Indels
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/strain="ATCC 30984"
                                                                                                                                                                                                                                                                                                                                                                         1230 York Avenue, New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                              Email: mmuller@rockvax.rockefeller.edu
Insert Length: 951 Std Error: 0.00
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The Rockefeller University
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Best Local Similarity 46.0%;
Matches 323; Conservative (
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/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
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                                               2334 GGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTA 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bapteste, E., Brinkmann, H., Lee, J. A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
756 CAAGGTCGCCGTCGTCGCGGCTACGGCGACGTGGGCAAGGGCTGCGCCGAGTCGCTGCG 815
                                                                                             816 CGCCAGGCTGCCGCGTCATCGTGACGGAGATCGACCCCATCTGCGCGCGTGCAGGCGTC 875
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45.3%; Pred. No. 0.00079;
Live 0; Mismatches 444; Indels 9;
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba
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/strain="ATCC 30984"
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1132 Std Error: 0.00
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                                                                                                                                      90 CATCAAGTGCTTCAACTGCGGCAAGGAGGCCCACATCGCCCGCAACTGCCGCGCCCCCCG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 CGGCCGCAACATGCTGACCCAGCTGGGCTGCACCTGAACTTCCCCCATCACCCCATCGA
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/strain="AMCC 30984"
/dLxref="taxon:108607"
/clone_lip="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
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          499 TGGAAGCCCAAGATGATCGCCGCCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAG
                                                                                                                                                    559 ATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCCACCCCC
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The Rockefeller University
1230 York Avenue, New York, NY 10021, UE
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1165 Std Error: 0.00
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Mastigamoeba balamuthi
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balamuthi cDNA similar to ribosomal protein S4, mRNA
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                                                                                                                                                                                                     Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 CCGCACAAGATGCGCGAGTGCCTGCCGGTCATCCTGCTGCGCAACAGGTTGAAGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAG 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 GCGCTGACCCGCCGTGAGGTCACCTCGATCGTGATGCAGCGCCTGATCAAGATCGACGGC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 ACCGACGAGCACTTCCGCCTGCTCTACGACACCAAGGGCCGCTTCCAGGCGCACCGCATC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AACTCGACCGAGGCCAAGTTCAAGCTCGGCAAGGTCCGCCGCGTGCAGCTCGGCAACAAG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 GGCATCCCGTACCTGGTGACCCACGACGCGCGACGATCCGCTACCCCAACCCCGACATC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 GCCCAGGGCACCCTGAACTTCCCCCAGATCACCCTGTGGGCAGCGCCCCCTGGTGAGCATC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 GAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGGATCGGCGGCATCGGCGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 TTCGAGATCGGCAACCTCGTCATGATCACTGGCGGACGCAACCTTGGCCGCGTCGGCGTC
                                                                                                                                     Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="ATCC 30984"
/db_xref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi lambda ZAP
/note="syn: Phreatamoeba balamuthi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 others
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Pred. No. 0.0012;
0; Mismatches 370; Indels

    1. 867
    /organism="Mastigamoeba balamuthi"

                                                                                                                                                                                                                                                                                                                                                                                                                                  1230 York Avenue, New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmuller@rockvax.rockefeller.edu
Insert Length: 867 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Biochemical Parasitology
The Rockefeller University
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                                                                 GI:18055836
                                                                                                                Mastigamoeba balamuthi
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Best Local Similarity 45.79
Matches 314; Conservative
                                                                 BM321430.1
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                                              ACCESSION
                                                                                                                                                                                REFERENCE
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                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mastigamoeba balamuthi"
/strain="ATCC 30984"
/dLxref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1761 CGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTG 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1821 GGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACTGGTGGAC 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1941 GAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCCGAGACCTTCTACGTGGA 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mastigamoeba balamuthi
Eukaryota: Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1550)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 CCACAAGGGGTTCGCGGCCGAGGACAACCCCAAGCTGCTGGAGGACGACGAGGGCCTCGA 244
                                                                                                           65 CGCCTGGAAGGGCGAGAACCTCCAGGAGTACTGGGAGTGCACCTGGAAGGCCCTGTGCTT 124
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                                                                                    655 GGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCC 714
ACCGTGCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTG 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 76.6; DB 13; Length 1550;
15.6%; Pred. No. 0.0032;
tve 0; Mismatches 364; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1550 Std Error: 0.00
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                                                                                                                                                                                                     715 GCCATGGACGCCCCAAGGTGAAGCAG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mastigamoeba balamuthi.
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Matches 308; Conservative
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                                                                                                                                                                                                                                                                                        RESULT 6
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HTC 25-MAY-2002
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1 (bases 1 to 2299)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

790 c 658 g 376 t
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GCAGAAGATCGTGAGCCTGACCGAGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCA 2120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design
                                                                                                                                                                                                                                                                                                                                                                                                                          602 GGAGATCGACCCCATCTGCGCTGCAGCGTGCGGGCTTCGAGGTCAACACACGCT
                                                                                                                                                                                                                                                                                                                     3301 CGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGA
                                                                                                                                                                                                                                                                                                                                                          542 CGACGTGGGCAAGGGCTGCGCCGAGTCGCTGCGGGCCAGGGCTGCCGCGTCATCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                 2361 CGGCATCGATGGCGGCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCGG
                                     305 GCACAAGATCCTCCCCGAGATCCGCGGTGTCAGCGAGGAGGACGACGACTGGCGTGATGAG
                                                                              GCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCT
                                                                                                                                                                                                                                                                            482 CATCAAGCGCGCCACCGACGTGATGCTCGGCGGCAAGGTCGCCGTCGTCGCGGGCTACGG
                                                                                                                                                                                                 425 TG---TCACCAAGAGCAAGTITGACAACATCTACGGCTGCCGCCACTCGCTCATCGACGG
                                                                                                                                                                                                                                      Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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Pred. No. 0.0052;
0; Mismatches 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/db_xref="MaizeDB:638374"
/db_xref="taxon:4577"
/clone="PCO142079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays PCO142079 mRNA sequence.
AY106831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2299 bp
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Unpublished (2002)
2 (bases 1 to 2299)
Coe, E.C.
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Best Local Similarity 43.0%;
Matches 734; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 CGAGGCGGGCTCGA 676
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                                  256 CGCTCCGACGCCACACGCTCCGACGTTTCGCGTGCGGCCATGCTCGTCGCAT
                                                                                                          316 CAACACCCTCCTCCAGGGCTACTCCGGCATCCGCTTCGAGATCCTCGAGGCCATCACCAA
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                                                                                                                                                                                                                                                                                                                                                                                               1620 CCA-----CGCCCTCGCCAGCGCGAGGCCGAAGGACGCCCAGCGCGTCTTCTC 1673
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1386 GTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACGACATCCA 1445
                                   1320 GAAGACCGCCGAGGCGGTGGACATCCTCAAGCTCATGTCGTCCACGTACATGGTCGCGCT 1379
                                                                       1446 GAAGCTGGTGGCCAAGCTGAACTGGGCCAGCCAGTCTACCCCGGCATCAAGGTGCGCCA 1505
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1 (bases 1 to 862)

1 bases 1 to 862)

Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                divergent amoebae: Dictyostellum, Entamoeba, and Mastigamoeba
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
21819461
                                                                                                                                                                                  1440 CGTGATGGCGGTGGCCAGGAAGGTGCTGACCACCAGCCTCGGCGGCGACCTCCACAGCGC
                                                                                                                                                                                                                       GGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGGGGCCCGTGCACGGCGTGTA
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Laboratory of Biochemical Parasitology
The Rockefeller University NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 862 Std Error: 0.00
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Mastigamoeba balamuthi
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1 (bases 1 to 3134)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
/strain="Arcc 30984"
/db_xref="taxon:108607"
/db_xref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi" lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi" others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1794 GATCGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCA 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1854 GAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTG 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1914 GGAGTICGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCAT 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2034 GGCCGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACAA 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2094 CCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGGGGGGGTGAA 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2271 GAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAG 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1734 CGCCAAGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAA 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1974 CATCGGCGCCGAGACCTICIACGIGGACGCGCCCCCAACCGCGAGACCAAGAICGGCAA 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 CATCGCGCAGGCCGGAGTCTCGGTCTTCGCCTGGAAGGGCGAGAACCTCCAGGAGTACTG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 GGAGTGCACCTNGAAGGCCCTGTGCTTCGGCCCCTACCAGGGACCTCAGANCATCGTCGA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 CGAGGAGACGACGACTGGCGTGATGAGGCTGTACCAGCTGCACGCGACGGCAAGCTGCT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     700 CTGCCGCCACTCGCTCATCGACGCCATCAAGCGCGGCACCGACGTGATGCTCGGCGGCAA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 CGCCAAGATCCGCTGGTGCTCGTGCAACATCTTCTCGACGCAGGACCACGCGGCCGCCGC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 CGACGGCGGTGACGCGACTCTAATGATCCACAAGGGGTTCGCGGCCGAGGACAACCCCAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2154 CATCGTGACCGACAGCCAGTACGCCCTGGGCATC---ATCCAGGCCCAGCCCGACAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 GITCCCGGCCGTCAACGTCAACGACTCTGTCACCAAGAGCAAGTTTGACAACATCTACGG
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                                                                                                                                                                                                                                                                                                              3.0%; Score 75; DB 13; Length 86 Similarity 46.2%; Pred. No. 0.0056; Conservative 0; Mismatches 327; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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8 Assemblies resulting from the application of public contigs to seed Dupont contigs, this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize of 448 294 354 567 414 687 747 115 GAGGGCCACATCGCCCGCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGC 174 175 AAGGAGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGAC 234 627 415 AAGGTGGCCGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTG 474 534 654 GGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCC 714 GGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGGAAGATCAAGGCCCTG 774 οĘ /organism="Zea mays"
/db_xref="MaizeDB:630364"
/db_xref="taxon:4577"
/clone="CL1506_1"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library" Design 389 ACGAGGCACCGCGACGCGTGGATCGAGCGGAACCCGTGCTGGTGAGGCTGACGGGA 235 CTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGC 295 CCCACCAGCCGCGAGCTGCAGGTGCGCGACAACCCCCGCAGCGAGGCCGGCGGCGAG 535 ATCAAGGIGCGCCAGIACGACCAGAICCIGAICGAGAICIGCGGCAAGAAGGCCAICGGC CCGGCGCCGCTGCACTACGTGCGCAACCACGCGCCGTGCCGCNNNNNACTGGGCGACG GCGCGCGACTTCCCCGCCGTGGAGATCCCCGTGACGCTGGCGTGCGCGGGGCAACCGGCGC 449 AGCACCGCTCAACTGCGAGCCGCCGCTAGCGCGGCTG-ATGCACCACGGCTTCATCACC 355 CGCCAGGGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATC 475 GAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTC 688 AAGGAGCAGAACAIGGIGCAGCAGGACGGIGGGCTTCAACIGGGGCGCCCCGGCGTGICC 748 ACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCGTGCTCCGCCGC---TGCGGCATCGTG 595 ACCGTGCTGATCGGCCCCCACCCCCGTGAACATCGTCGGCCGCAACATGCTGACCCAGCTG NNNNNNNNNNNGTACGGCACCAGCGTCACGCGCGAGTGGGCCCTGGACCCGGTCGCGGGGAC Submitted (25-APR-2002) Maize Mapping Project, University Missouri, Columbia, MO 65211, USA Location/Qualifiers Length 3134; Maize Mapping Project/DuPont Consensus Sequences for 181 others 0; Mismatches 1347; Indels 3.0%; Score 74.4; DB 11; 40.6%; Pred. No. 0.0077; 467 t 916 9 Mapping Project" 982 c 916 Overgo Probes Unpublished (2002) 2 (bases 1 to 3134) Best_Local Similarity 40.6 Matches 963; Conservative Direct Submission Coe, E.C. Query Match source BASE COUNT 508 TITLE JOURNAL JOURNAL REFERENCE 628 AUTHORS FEATURES TITLE ORIGIN ô ò g à qq q g g g à õ ò ŏ g ŏ Dp ò a ò

1422 1482 1101 1161 1014 1074 1281 1341 1194 1254 1461 1581 1767 1401 1521 1701 1761 1828 ACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAG--------ACC 1863 985 CGCGTCATCATCCCCGGCTGCATCGGTGGCCGCATGGTCAAGTGGCTCAAGCGC---ATC 1041 1822 GACCACCCCGGCGCGCCGACAGCATCCTCATCAACGCCGGCACCGACTGCACCGAGGAG 1881 1882 TTCGACGCCATCCACTCCGACAAGGCCAAGGCGCTCCTCGACACCTACCGCATCGGCGAG 1941 834 1522 AACTGCTGCTTCAAGGTGAAGGTGAACGTGTGCCGTCCGCACAAGGCCGAGATCGGGCTG 775 ACCGCCATCTGCGAGGAGATGGAGAAGGAGGCCAAGATCACCAAGATCGGCCCCGGAGAAC 1042 ATCGTCANNNNGCCGAGTCCGACAATTACTACCATTTCAAGGACAACCGCGTCCTGCCG 1102 TCGCACGTCGACGCCGAGCTCGCCAACGCAGAAGCGTGGTGGTACAAGCCGGAGTACATC 1015 TACTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGC 1222 ATCAACAGCATTACCACACAGGGGGGTACAACGAAAGGATACGCCTACTGGGGGG 1075 ATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAG 1195 AACCCCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCCAGCGACCTGGAG 1402 TCCGTCGAGGTGGAGGTCCTCGACCTGCTCGCCGCCAAGGAGATCGCCGTGCCGCATGG 1255 ATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGTGGGGCTTC 1462 GACCAGTCGCTCAACACCCAGCCCGAGAAGCTCATATGGAACCTCATGGGATGATGAAC 1375 CACCCCGACAAGTGGACCGTGCAGCCCATCGAGC------TGCCCGAGAAGGAG 1582 GTGTTCGAGCCACCCGACGCAGCCCGGCAACCAGCCCGGCGGGGGATGGCGCGGCGGCAGAG 1543 GACATCGTGCCCTGACCGAGGGCCGAGCTGGAGCTGG-----CCGAGAACCGCGAG 1597 ATCCTGCGCGGAGCCCGTGCACGGCGTGTACTACGACCCCCAGCAAGGACCTGGTGGCCGAG 1942 CTCATCACCACGGGCACCGGCTACAGCTCCGACAACTCCGTCCACGGCGGCGCTCCTG 1768 AAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAG 2002 TCGCACCTCGCGCCCATCCGCGAGGCCGTCAGGGNNNNNGCGCTCTCCAACCCGCGCGAT 835 CCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTG 895 GTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATC 955 CCCCACCCCGCCGGCCTGAAGAAGAAGAGGGGTGACCGTGCTGGACGTGGCGACGCC 1162 ATCAACGAGCTGAACATAAACTCGGTGATAACGACGCCGGGGCACGACGAGATCCTGCCC 1135 GGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGC 1342 CACCTCGACCACCCGGAGAAGCCCAACAAGTACGGCAAGTACTGGTGCTGGTGCTTCTGG 1315 ACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTG 1762 CAGGAGTCGGCGTGCATCGCCGTGCACGGCCACGTCTACGACTGCACCAAGTTCCTCAAG 1657 ATCCAGAAGCAGGCCACGACCACGACCTACCAGATCTACCAGAGCCC-----1708 TTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCACACCAACGACGTG g q δy g Db δŽ g QY δ q QΥ g δy qq δy g Öλ Dp δλ qq δy q g Db g g g Óγ δ δ δ ΩŽ ò ò QΣ

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807 541 867 595 655

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BMS87428 566 bp mRNA linear EST 25-FEB-2002 17000687321202 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449696110 5', mRNA sequence.
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Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
                                                           II Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        868 AAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGGAGCTGAACAAGCGCACCCAG 927
                                                                                                                                                                                                                                   CTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTG 447
                                                                                                                                                                                                                                                                                                                                                                                                                          245 CTGCTCGACGTCGGCCTGGTCCGCACCTCGACCGGCGCCCCGCGTGTTCGCCGCCCTCAAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AACGGCGACAAGAAGGAGCTCAACGCCGCGGTCCTCCGCAAGTACATCTTCGGCGGCCAC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Greececeracardaagerecreaagaageagaagacececececerreaaceagric 481
                                                                                                                                                                                                                                                                      125 CTGGCCCGCCGTGTGCTGAAGAAGCTCAACCTCCAAGTACGAGGGTGTCAAGAAG 184
                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                            448 GACACCGGCGCCGACGACACCGTGCTGGAGATGAGCCTGCCCGGCAAGTGGAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                        508 AAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 GGCATGTGCGACGGCGCGCGTCAACGTCCCC---CACAGCGAGACCCGCTTCGTCGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   928 GACTICIGGGAGGIGCAGCIGGGCATCCCCCACCCGGCCGGCCTGAAGAAGAAGAAGAGC
                                                                                                                                                                                                                                                                                                                                    GAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCGGTGAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         628 ATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCCATCAGCCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     688 GAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGCCCCCAAGGTGAAGCAGTGGCCC
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                                                                                                                                                                                               6
                                                           ZAP
                                                                                                                                                         Length 853
                                                           balamuthi lambda
balamuthi"
                                                                                                                                                       3.0%; Score 73.2; DB 13; Length 46.9%; Pred. No. 0.011; tive 0; Mismatches 329; Indels
/organism="Mastigamoeba balamuthi"
/strain="ATCC 30984"
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/clone_lib="Mastigamoeba
/note="syn: Phreatamoeba
307 c 263 g 125
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                                                                                                                                                                                             299; Conservative
                                                                                                                                                                             Similarity
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                                                                                                                                                         Query Match
                                                                                                                                                                             Best Local
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BM587428/c
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ORGANISM
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KEYWORDS
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Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The analysis of 100 genes supports the grouping of three highly divergent amoebbe: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002) 21819461
1924 AACACCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCC 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCGAGGTG 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCGTGTACGCCAACCGGACGGACGACATCCTCCTCCGCGACGACGACCGGTGG 2598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2599 GCGCCCAGTACCCGGACACGCTCAAGGTGGTACGTCCATCGACCAGGTAAAGCCCCG 2658
                                                       TGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTG 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
                                                                                                                                                                                                                                   2344 AAGGTGCTGTTCCTGGACGCCATCGATGGCGGCATCGTGATCTACCAGTACATGGACGAC
                                                                                                                                                                     2182 receccaccarreaagegaagererecargegegerarcaceccaccagearerecac
                                                                                                                                                                                                               GAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTAC
                                                                                                                                                                                                                                                                                          TICCCCAACGGCGCCTCATGACCCAGTACCTCGACTCGCTTCCCGTCGGCGCCTACATC
                                                                                                                                                                                                                                                                                                                                                                  GAGCTGCAGCCCATCCAGCTGGCCCTTGCAGGACAGCGGCGAGCGTGAACATCGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAAGCAGCGCCATGCGAGCCGCCTCGCCATGATCTGCGGCGGAAGTGGGAATCACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2284 GCCCACAAGGGCATCGGCGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCC
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1 (bases 1 to 853)
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 853 Std Error: 0.00
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Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T. Full length cDNA of Dictyostellum discoideum at the culmination
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                                                                                                                                                                                                                                                                                                                                                                                         /clone="ddc18f13"
/clone_11b="Dictyostellum discoideum cDNA library, CF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1108 TACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACC 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568 GAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCCGTGAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561 NTNATCANGATGAAGNAGCNGAAGNTGTTNATCANGNTGAAGTAGTTGATNNNGTNGNNG
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                                                                                                                                                                                                                                                                                                                       /organism="Dictyostelium discoideum"
                                                                                                          Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
III Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Bmail: tshini@enes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72.4; DB 13;
Pred. No. 0.015;
0; Mismatches 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Culmination stage"
103 c 137 g 240 t
                                                                                                                                                                                                                                                                                                                                               /strain="AX4"
/db_xref="taxon:44689"
                                                                                                                                                                                                                                                    tshini@genes.nig.ac.jp.
Location/Qualifiers
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ilarity 36.5%;
Conservative
  (bases 1 to 801)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ375394 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc18f13 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1956 GCTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCCCCAACCG 2015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 CATGATCAAGGATGCGGAGCGGTTCGCCGACGACGAGAAGAAGCTGAAGGAGCGCGTGGA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 CAAGCTGGGCGCGAGCGTCCGACGACGACGAGGCCAAGGTGGAGGCGATCGACGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 GTTCGAGATCGACGCCAACGGCATCCTGCAGGTGTCGGCCGAGGACAAGGGCACGGGCAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 GAAGATCAAGTGGCTGGACGAGAACCAGGACACCGAGGCGGAAGAAGTACAAGAAGCAGAA 123
                                                                                                                                                                                                                                                                                                 /strain="RSP-ST (Reduced susc. to Permethrin - std
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 CCGGGAAAAGATCGTCATCACCAACGACCAGAACCGCCTGACGCCGGACGACATCGAGCG
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Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                               /clone="19600449696110"
/clone=1Pb="A.gam.ad.cDNA.blood1"
/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72.8; DB 13;
Pred. No. 0.013;
0; Mismatches 217;
                                                                                                                                                                                                                                                                          /organism="Anopheles gambiae"
                     Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, 17el: 2404533151
Email: HoltRA@celera.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 t
  Celera Anopheles gambiae EST project
                                                                                                                                                                                  Plate: NU01004AAX row: G column:
Seq primer: M13 Reverse.
Location/Qualifiers
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R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Gelera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 GGCCGCAACGAGCTCGAGAGCTACGCGTACACCTGAAGAACCAGCTCGAAGGA 288
Eukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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chromosome)"
                                                                                                                                                                                                                 M645449 646 bp mRNA linear EST 26-7000687316588 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 9600449648747 5', mRNA sequence.
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Tel: 2404533151
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/clone="19600449648747"
/clone_lib="A.Gam.ad.cDNA1"
/dev_stage="Adult"
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Plate: NU01004920 row: B column:
Seq primer: M13 Reverse.
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194 c 210 g
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                                                                                                                                                                                                                                                                                                                                                 African malaria mosquito.
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BMS84191 724 bp mRNA linear EST 22-FEB-2002 17000687279987 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19000449683331 5', mRNA sequence.
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Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab , R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
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                                                                                                                                                                                                     2316 CGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGG 2375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1956 GCTGGAGAAGGAGCCCATCATCGGCGCGGAGCCTTCTACGTGGACGGCGCCGCCAACCG 2015
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2196 CCAGCCCGACAAGAGCGAGGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAA 2255
                                             289 CAAGCTGGGCGCGAGCGTGTCCGACGACGACGACGAGGCCAAGATGGAGGAGGCGATCGACGA 348
                                                                                                                               224 GTTCGAGATCGACGCCAACGCCATCTGCAGGTGTCGGCGAGGACAGGGCACGGGCAG 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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chromosome)"
                                                                                                  2256 GGAGAAGGIGTACCTGAGCTGGCTGCCCGCCCACAAGGGCATCGGCGCGCAACGAGCAGAT
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/clone=lib="A.Gam.ad.cDNA.blood1"
/de_stagge="Adult"
/lab_host="DH10b"
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Tel: 2404533151
Fax: 2404534580
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Plate: NUG1004B2V row: B column:
Seq primer: M13 Reverse.
Location/Qualifiers
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Contact: Holt R.A.
Celera Genomics
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Eukaryota; Metazoa
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SOURCE
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864 SCTSSACVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSG 805

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                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit AL053013
                                                  2255
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2136 CAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGC 2195
                                                                                                                  404 GGCCGCCAACGAGCTCGAGAGCTACGCGTACAGCTGAAGAACCAGCTCAGCTCGAAGGA 463
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                         464 CAAGCTGGGCGCGAGCGTGTCCGACGACGACGAGGCCAAGATGGAGGAAGCGATCGACGA
                                                                                                                                                    2316 CGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGG
                                                 2196 CCAGCCGACAAGAGCGAGGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAA
                                                                                                   2256 GGAGAAGGTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGAT
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/db_xref="taxon:7227"
/clone="BACR19D16"
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15.6%; Pred. No.
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/note="end : TET3"
61 c 61 g
                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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Matches 58; Conserv
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CNS0091P/c
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TITLE
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                                                                                                                                                                                                                                                                                             ACCESSION
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KEYWORDS
SOURCE
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 10, 2003, 12:14:58; Search time 80.1949 Seconds Run on:

(without alignments) 9441.811 Million cell updates/sec

1 gtcgacgccaccatggccga......gggctagcaccggtgaattc 2469 US-09-610-313-30 2469 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

441362 seqs, 153338381 residues Searched:

882724 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Issued_Patents_NA: * Database

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | I and 7 equality | - σ | , [| | Sequence 9. | Seguence 5. | Sequence 1, | Sequence 1, | Sequence 15, | Sequence 13 | 3 Sequence 33. | Sequence 35. | Sequence 35. | Sequence 7. | Sequence 7 | Sequence | Sequence 3, | Sequence 3, | Sequence 1, | Sequence 4, Appl | 3, | 4 | 6 | Ή, | · | Sequence 1, Appl | Concept 5 |
|-----------|------------------|------------------|-----------------|-------------|-------------|---------------|-------------|-------------|-------------|---------------|-------------|----------------|--------------|--------------|-------------|------------|----------|-------------|-------------|-------------|------------------|--------|--------|------------------|--------|-----------|------------------|-----------|
| SUMMARIES | ID | US-09-117-217-7 | US-09-117-217-9 | -09-117-217 | -09-117-217 | -08-418-848A- | -188-5 | -08-38 | -488-551B- | -09-309-572-1 | 12-1 | -848-760B- | -646-538-3 | -503-222-3 | -94 | .35 | - 80- | .38 | -64 | -12 | 80 | 60- | -06 | US-09-620-958A-9 | -08 | -388-809- | US-08-647-714-1 | -08-463- |
| | Length DB | 2601 4 | 2601 4 | 2601 4 | 2601 4 | | | | 9709 3 | | 12494 4 | 12494 4 | | 15581 4 | 9737 2 | • | 9746 1 | | | | | • | 8933 4 | 8933 4 | 9739 1 | | 9739 2 | . , |
| ď | Query Match I | 45.8 | | | | 45.6 | | | 45. | 45. | 45. | 45. | 45.6 | | | | 43.8 | | | | | m. | | | | | 43.2 | |
| | Score | 1132 | 1132 | 1132 | 1132 | 1125.6 | 1125.6 | 1125.6 | 1125.6 | 1125.6 | 1125.6 | | 1125.6 | 1125.6 | 1116 | 1116 | 1080.8 | 1080.8 | 1080.8 | 1079.6 | 1079.6 | 1079.6 | 1079.6 | 1079.6 | 1067.2 | 1067.2 | 1067.2 | o |
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| Seguence 19, Appl | 21, 7 | | 800, | 20. A | Sequence 16, Appl | 1 . | Sequence 1, Appli | | 56. | Sequence 56, Appl | Sequence 56, Appl | 56. | 1 | Sequence 18. Appl | Sequence 14. April | 4 | Sequence 14, Appl |
|-------------------|------------------|-------------------|--------------------|------------------|-------------------|------------------|-------------------|-----------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|--------------------|------------------|-------------------|
| US-07-743-357-19 | US-07-743-357-21 | US-08-388-353-800 | US-08-488-551B-800 | US-07-743-357-20 | US-07-743-357-16 | US-08-876-546A-1 | US-09-412-252-1 | US-09-079-675-1 | US-08-470-202-56 | US-08-471-770-56 | US-08-468-059-56 | US-09-109-916-56 | PCT-US93-06748-1 | US-09-158-695-18 | US-08-659-251-14 | US-09-256-490-14 | PCT-US96-11445-14 |
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ALIGNMENTS

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4
                                                GENERAL INCORMATION:
APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: PAUGES, Rud;
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: DF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 TCAAGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130
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45.8%; Score 1132; DB 4; Length 2601;
Best Local Similarity 68.5%; Pred. No. 8.6e-178;
Matches 1626; Conservative 0; Mismatches 730; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)..(492)
; OTHER INFORMATION: gag Polyprotein
US-09-117-217-7
                    ; Sequence 7, Application US/09117217
; Patent No. 6221578
                                                                                                                                                                                                                                                                                                                                              ORGANISM: HIV-HXB2
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| Oy Dp | 311 | TGCAGGTGCGCGGCGACAACCCCGCAGGCGGGCGGGCGGCGGCGGCGGCAGGGCAATTTTTTTT | 364 435 |
| Qy Db | 365 436 | CCCTGAACTTCCCCCAGATCACCCTGTGGCAGGCCCCCTGGTGAGGGCATCAAGG | 418 495 |
| Qy Db | 419 | TGGGCGGCCAGATCAAGGAGCCCTGCTGGACACCGGGCGCCGACGACGACGACGACGACGACTGCTGGAGGAGTTAAAGAAGTCTATTAGATACAGGAGCAGATGATACAGATACAGGAGCAGATGATAGAAGCAACTATTAGATACAGGAGCAGATGATACAGAAGCAACTATTAGATACAGGAGCAGATGATACAGATACAGGAAGCAACTATTAGATACAAGGAAGCAACAATAAAAGAAGCTCTATTAGATACAAGGAAGCAACAATAAAAGAAGCTCTATTAGATACAAGGAAGCAAGATACAAGAAGAAGAAGATAAAAAGAAGCAAAGATACAATAGATACAAGAAGCAAGATAAAAAGAAGAAGCTCTATTAGATACAAGAAGCAAGATACAAGAAGAAAGA | 478 |
| 0y | 7 | AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCA | ر |
| G & 6 | | ANGIGGCCAGTACGAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCCC | 1 0 1 |
| 69 10 10 10 10 10 10 10 10 10 10 10 10 10 | 1 6 1 | SATCGGCCCCACCCCGGGACATCATCGCCGCAACATGCTGACCCAGCTGGGACTTGTGATTTTTTTT | വ വ |
| Qy | 659 | GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA | |
| Qy Db | 719 | TGGACGGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGGGGAGAAGATCAAGGCCCTGACCG | 778 |
| Qy | 779 | CCATCTGCGAGGAGATGGAGAGGGCAAGATCACCAAGATCGGCCCGGAGAACCCCT | 838 915 |
| Qy Db | 839 | ACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGTTTTTTTT | 898 |
| Qy Db | 976 | ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC | 958 1035 |
| Qy Db | 959 | | 1018 |
| Oy Db | 1019 | | 1078 |
| Qy Db | 1079 | ACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA | 1138 |
| Qy Db | 1139 | GCCCAGCATCTTCCAGAGCAGGATGACCAAGATCCTGGAGCCCTTCCGGGCCCGCAACC | 1198 |
| Qy | 1199 | | 1258 |
| Qy | 25 | GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGCTTCACCA | 31 |
| 9 6 | 1319 | | 1378 |
| . g | 39 | | 45 |
| Qy | 1379 | CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGGTGGACCGTGAACG | 1438 |

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1456 CTGATAAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAAGACAGCTGGACTGTCAATG 1515
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                                     1499 TGCGCCAGCTGTGCAAGCTGCTGCGGGGGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGA
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Sequence 9, Application US/09117217 Patent No. 6221578

; Sequence 9, Applicat: ; Patent No. 6221578 ; GENERAL INFORMATION:

RESULT 2 US-09-117-217-9

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APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: HERTGGS, Kurt
APPLICANT: PAUWELS, Kurt
APPLICANT: PAUWELS, Kurt
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: OF HUMAN HIV STRAINS
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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                                                                                                                                                                                                           Length 2601;
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                                                                                                                                                                                                         45.8%; Score 1132; DB 4;
68.5%; Pred. No. 8.6e-178;
tive 0; Mismatches 730;
                                                                                                                                                        NAME/KEY: CDS
LOCATION: (334)...(489)
OTHER INFORMATION: gag P6 (52 AA)
                                                                                                                                                                                                                             Matches 1626; Conservative
                                                                                                                                                                                                                    Similarity
                                                                                                                                        ORGANISM: HIV-HXB2
                                                                                                                    2601
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                                                                                                                               TYPE: DNA
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APPLICANT: HERTOGS, KUTT
APPLICANT: HENTOGS, KUTT
APPLICANT: PADWELS, RUGI
TITLE OF INVENTION: MTHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: HV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VEF. 2.0
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Pred. No. 8.6e-178;
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Patent No. 621578
GENERAL INFORMATION:
APPLICANT: de BETHUNE, Marie-Pierre
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LOCATION: (453)
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US-09-117-217-11
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APPLICANT: de BETHUNE, Kurt
APPLICANT: HERTOGS, Kurt
APPLICANT: HERTOGS, Kurt
APPLICANT: PAUWELS, Rudi
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: DE HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILLNG DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
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ilarity 68.5%; Pred. No. 8.6e-178;
Conservative 0; Mismatches 730;
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                                                                                                                                                                       Sequence 13, Application US/09117217
Patent No. 6221578
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                                                              1739 AGATGCGCACCGCCCACAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
                                                                                                                                                                                                                                                                1996 ITGITAATACCCCTCCCTTAGTGAAATTATGGTACCAGTTAGAGAAACACATAGTAG
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                       1619 GCGTGTACTACGACCCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC
                                                                                                  1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA
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HARMISON II, IE, CHEN, BANJERJEA, AKHIL

GENERAL INFORMATION:
APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: GEORGE G., CHANG-JIE, CHEN, BAN
TITLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77

Sequence 9, Application US/08418848A Patent No. 5847096

RESULT 5 US-08-418-848A-9 ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE

NEW YORK
RY: U.S.A.
10154

CITY: NEI COUNTRY:

CORRESPONDENCE ADDRESS:

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IGGCIGAAGCAATGAGCCAAGTAACAAATCCAGCTACCATAATGATACAGAAAGGCAATT 1897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1125.6; DB 2; Length 7399;
Pred. No. 1.1e-176;
0; Mismatches 734; Indels 16;
                                                                                                                                                                                                                                                                        2026-4091US2
                                                           SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,848A
FILING DATE: 07-APR-1995
CLASSIFICATION: 526
PRIOR APPLICATION DATA:
                 MEDIUM TYPE: Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                    APPLICATION NUMBER: 07/936,849
                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFRAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 7399 base pairs TYPE: nucleic acid STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity 68.48;
                                                                                                                                                                                    FILING DATE: 28-AUG-1992
CLASSIFICATION: 526
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1622; Conservative
COMPUTER READABLE FORM:
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Best Local
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                                                           GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCCA
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                                                                                                   3577 GAATGAAGGGTGCCCACACTAATGATGTGAAACAATTAACAGAGGCAGTACAAAAATAG
                                                                                                                                            CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG
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                                                                                                                                                                                                                              1859 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/188,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Desrosiers, Ronald C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 F
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-188-583-5
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                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1e-176;
                                                                                                                 Reg. No. 5851813 29,066
                                                                                                                                       00246/079002
          FILING DATE: July 9, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/551,945
FILING DATE: July 12, 1990
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 07/727,494
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                       68.4%;
                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 68.4
Matches 1622; Conservative
                                                                                                    NAME: Freeman, John W. REGISTRATION NUMBER: R
                                                                                                                                                                                        TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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linear
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US-08-188-583-5
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TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGGAAGATCAAGGCCCTGACCG 778
                                                                                                                        ACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG 898
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3676 CCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAATTACCCATACAAAAGG 3735
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APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2339 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08388353
Patent No. 6010895
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REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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ZIP: 11530
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STREET: 40
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                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                     Length 9709
                                                                                                                                                                                                                                                                        Score 1125.6; DB 3; Length
Pred. No. 1.1e-176;
0; Mismatches 734; Indels
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                        Query Match 45.6%;
Best Local Similarity 68.4%;
Matches 1622; Conservative
                                                                                                                                                                                    linear
                                                                                                                                                                               TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-388-353-1
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ACAATACTCCAGTATTTGCCATAAAGAAAAAGACAGTACTAAATGGAGAAAATTAGTAG 2775
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3796 TTGTCAATACCCCTCCCTTAGTGAAGTTAFGGTACCAGTTAGAGAAAGAAAGCCCATAATAG 3855
                                 1979 GCGCCGAGACCTTCTACGTGGACGGCGCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
                                                  TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCG
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APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
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ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      2339 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388, 353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
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07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08488551B Patent No. 6015661
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (516) 742-4343
(516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 07-JUN
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US-08-488-551B-1
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                                                                                                                                                                                                                                                           734; Indels
                                                                                                                                                                                                          45.6%; Score 1125.6; DB 3;
llarity 68.4%; Pred. No. 1.1e-176;
Conservative 0; Mismatches 734;
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                   SEQUENCE CHARACTERISTICS:
LENGTH: 9709 base pairs
INFORMATION FOR SEQ ID NO:
                                                                  nucleic acid
EDNESS: single
                                                                                                                                                                                                                                  Similarity
                                                                                                                   linear
                                                                                                                                       MOLECULE TYPE: DNA US-08-488-551B-1
                                                                                        STRANDEDNESS:
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                   899 ACTICCGCGAGCIGAACAAGCGCACCCAGGACTICTGGGAGGIGCAGCIGGGCAICCCCC
                                                                            1379 CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGGTGGACCGTGAACG
                                                            ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGGACGTGGGCGACGTACT
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                                                                             3916 GATATGTAACTGACAGAGGAAGACAAAAAGTTGTCCCCCTAACGGACACAACAATCAGA
                                                                                                             AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCGCAGCGAGGTGAACATCG
                                                                                                                                                                                                                                                           TGAAGGACTGCACCGAGCCCAAGTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG
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Pred. No. 1.1e
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CURRENT FILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09309572 Patent No. 6440730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
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Best Local Similarity 68.44
Matches 1622; Conservative
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US-09-309-572-15
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                                                                                      419 TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCCGACGACACCGTGCTGGAGG
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                                                                                                                                          AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGTCGGCGGCTTCATCA
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                             ACAICCAGAAGCTGGTGGCCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGG 1498
                                                         ACATACAGAAATTAGTGGGAAAATTGAATTGGGCAAGTCAGATTAATGCAGGGATTAAAG 3375
                                                                                                      CCGAGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGAGCCCGTGCACG
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; Sequence 13, Application US/08935312; Patent No. 6207455; GENERAL INFORMATION: APPLICANT: CHANG, Lung-Ji

US-08-935-312-13

RESULT 10

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                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
                                                     E: BROWDY AND NEIMARK, P.L.L.C 624 Ninth Street, N.W.
LENTIVIRAL VECTORS 20
                                                                                                                                                                                                                                                                   US/08/935,312
                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = ""DNA""
                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
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nucleic acid
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202-737-3528
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.45
Matches 1622; Conservative
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                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                      Washington
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                                                                                                                         COUNTRY:
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                                                           659 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCGGTGAAGCTGAAGCCGGGA
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                                      539 AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCCATCGGCACCG
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                                                                                                                                    AGATGCGCACCCCCACCACCAACGACGTGAAGCAGCTGACGAGGCCGTGCAGAAGATCG 1798
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AGACTGAGTTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAACATAG
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TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/08848760B Patent No. 6248721 GENERAL INFORMATION:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.6%; Score 1125.6; DB 4; Best Local Similarity 68.4%; Pred. No. 1.1e-176; Matches 1622; Conservative 0; Mismatches 734;
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CNG-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                          NAME: PACE, DORAN R. REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12494 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                               TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
                                                             TGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG
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APPLICANT: Stauber, Roland H.
APPLICANT: Stauber, Roland H.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
                                                                                                                                                                                                                                                                                                                                                                                                              3647 AGACTGAGTTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAAACATAG
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                                      3287 GAATGAAGGGTGCCCACACTAATGATGTGAAACAATTAACAGAGGCAGTACAAAAATAG
                                                                            CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG
                                                                                                  1859 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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PatentIn Release #1.0, Version #1.30
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No. 6027881 yet assigned
1: 435
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MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ADDRESSEE: Townsend
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STATE: California
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FILING DATE: NO. 60:
CLASSIFICATION: 435
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                                                                                                                                                                                                                Length 15581;
                                                                                                                                                                                                             Score 1125.6; DB 3; Length
Pred. No. 1.1e-176;
0; Mismatches 734; Indels
                               015280-249000
                                                                                                                                                                                /note= "pNLnSG11'
       NAME: Weber, Kenneth A.
REGISTRATION UNDRER: 31,677
REFERENCE/DOCKET UNDRER: 01528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 15581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                              45.6%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  Matches 1622; Conservative
                                                                                                                                                     NAME/KEY: - 1..15581
                                                                                                                                                                   ; LOCATION: 1..15581; OTHER INFORMATION: US-08-646-538-35
                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA
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APPLICANT: Gaitanaris, George A.
APPLICANT: Gatuber, Roland H.
APPLICANT: Stauber, Noun N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
CORRESPONDENCE ADDRESS:
                                                                                                            1859 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
                                                                                            1979 GCGCCGAGACCTTCTACGTGGACGGCGCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
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APPLICATION NUMBER: US/09/503,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2339 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
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APPLICATION NUMBER: US/08/646,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application US/09503222
Patent No. 6265548
GENERAL INFORMATION:
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94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-503-222-35
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                                                                                                                                                                                                                                                                                                                                                                                                          45.6%; Score 1125.6; DB 4; Length 15581;
68.4%; Pred. No. 1.1e-176;
Live 0; Mismatches 734; Indels 16; (
015280-249000
                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: /note= "pNLnSG11" US-09-503-222-35
               TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 15581 base pairs
TYPE: nucleic acid
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 1622; Conservative
                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         NAME/KEY: -
LOCATION: 1..15581
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TYPE: DNA ORGANISM:
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                                                                                                               ACTITCCGCGAGCTGAACAAGCGCACCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC 958
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APPLICANT: WERNER, ALBRECHT
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: UNBER: US/08/944,449
CURRENT APPLICATION NUMBER: US/08/944,449
CURRENT FILING DATE: 1997-10-06
EARLIER FILING DATE: 1995-08-18
EARLIER FILING DATE: 1995-04-07
NUMBER: OF SEQ ID NOS: 8
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3736 AAACATGGGAAGCATGGTGGAAGTATTGGCAAGCCACCTGGATTCCTGAGTGGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08944449 Patent No. 5985613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; GENERAL INFORMATION:
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2003 2122 2182 2242 2422 2482 2542 2602 2662 2722 2842 1078 3023 CACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAACAGAATC 3082 1139 GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC 1198 250 310 418 478 538 598 658 718 778 838 868 958 1944 TTAGGAACCAAAGAAAGACTGTTAAGTGTTTCAATTGTGGCAAAGAAGGGCACATAGCCA 2123 GGAAGGCCAGGGAATTTTCTTCAGAGCAACCAGAGCCAACAGCCCACCAGAAGAGAGC TGAAGGACTGCACCGAGCCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG GCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCCAACAGCCCCAACAGCCGCGAGC 365 -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGG TGGGCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGG 2303 TAGGGGGCCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAG AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCGTTCATCA 539 AGGTGCGCCAGTACGACCAGATCCTGATCTGCGGCAAGAGGCCATCGGCACCG 2483 TATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTGGTT GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA 719 TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG CCATCTGCGAGGAGGAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT 2663 AGATATGTACAGAAATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAAAATCCAT ACAACACCCCCGTGTTCGCCATCAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG 899 ACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC ACCCCCCCCCCCGCCTGAAGAAGAAGAAGAGCGTGACCTGCTGGACGTGGGCGACGCCTACT ACCCCGCAGGGTTAAAAAAAAAAATCAGTAACAGTATTGGATGTGGGTGATGCATACT 1019 TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCATCCAGCATCA TTCAGTTCCCTTAGATAAAGACTTTAGAAAGTATACTGCATTTACCATACCTAGTATAA ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCCAGGGCTGGAAGGGCA GCAACTGCCGCCCCCCCCCAAGAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCAACAAA 599 TGCTGATCGGCCCCACCCCGGTGAACATCGGCCGCGCAACATGCTGACCCAGCTGGGGCT 311 479 629 959 2843 2903 1079 131 191 251 419 779 839 q Dp qq q Dp Dp g οy g g QΥ δy ò Pp Qγ οy ò g δy g QQ a Qγ g ò g ŏ ò δ δy οy Q

1918 4162 1318 1438 1498 3442 1618 3502 1678 1738 3682 1858 1978 3862 2038 3922 2098 2158 3802 3563 AATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATGCAA 3923 GATATGTTACTGACAGAGGAAGACAAAAAGTTGTCTCCATAGCTGACACAAAATCAGA | CCAGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG 3143 GGCAGCATAGAACAAAAATAGAGGAACTGAGACAGCATCTGTTGAGGTGGGGGATTTACCA CCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCTGGATGGGTACGAGGTGCACC 3203 CACCAGACAAAAAACATCAGAAAGAACCTCCATTCCTTTGGATGGGTTATGAACTCCATC 1379 CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG ACATCCAGAAGCTGGTGGGCAAGCTGAACTTGGGCCAGGCCAGATCTACCCCGGCATCAAGG 3323 ACATACAGAAGTTAGTGGGAAAATTGAATTGGGCAAGTCAGATTATGTGCAGGGATTAAAAG 1499 TGGGCCAGCTGTGCAAGCTGCTGCGGGGGCCCAAGGCCCTGACCGACATCGTGCCCCTGA 3383 TAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAA 1559 CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGGCCCGTGCACG 1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1739 AGATGCGCACCGCCCACAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG 1799 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 3683 CCACAGAAAGCATAGTAATATGGGGAAAGATTCCTAAATTTAAACTACCCATACAAAAGG 1859 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT 1919 TCGTGAACACCCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCCATCATCG 1979 GCGCCGAGACCTTCTACGTGGACGGCGCCCAACCGCGAGACCAAGATCGGCAAGGCCG 3863 GAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGGGAGACTAAATTAGGAAAAGCAG 2099 AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCG 3983 AGACTGAATTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAAACATAG TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCG 4043 TAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAAACCAGATAAGAGTGAATCAG 2219 AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG GCCAGCACCGCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCTGCGGGCCTTCACCA 1619 GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 3503 AAGTATATTATGACCCATCAAAAGACTTAGTAGCAGAAATACAGAAGCAGGGGCAAGGCC 1319 1439 2039 2159 1199 1259 QQ Db qq QQ qq g QQ qq g qq qq g OD ŏ QΫ QΥ $\dot{\Omega}$ QΥ ŏλ q QΥ δ QY Qγ QΫ οg ŏ g g δλ g ò Q Qγ

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                                                                                                                                                                 Use of an "immunodeficiency-virus suppressing
lymphokine (ISL)" to inhibit the replication of viruses,
in particular of retroviruses
2279 IGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCA 2338
              TCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9737;
                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 4.1e-175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     740;
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                                                2339 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 13 152.5
FILLING DATE: 07-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95113013.2
                                                                                                                                      US/09353362
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: KLESNER, Sharon N. REGISTRATION NUMBER: 36.335 REFERENCE/DOCKET NUMBER: PARTECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-353-362-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9737 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                    TITLE OF INVENTION: UTITLE OF INVENTION: 1
TITLE OF INVENTION: 1.
NUMBER OF SEQUENCES:
                                                                                                                                    Sequence 7, Application Patent No. 6383739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1616;
                                                                                                                          US-09-353-362-7
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Best Local 3
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2123 GGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGC 2182
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                                                                                                       2303 TAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2483 TATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             719 TGGACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2663 AGATATGTACAGAAATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAAAAATCCAT
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                                                                 311 TGCAGGTGCGCGGGGG-----ACAACCCCCGCAGCGAAGGCCGGCGCGGCGAGCGCCAAGGGCA
                                                                                                                                                                                                 -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGG
                                                                                                                                                                                                                                                                                                                                    TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACGCCGGCGCGGACGACACCGTGCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 AGATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGATCGGCGGCGATCGGCGGCGTTCATCA
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1379 CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGA 1558
                                                                                                                                                                                                       1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA
                                                                                                                                                                                                                                                                                                   TCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGAAGAGCCCATCATCG
                                                                                                                    3383 TAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAA
                                                                                                                                           CCGAGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCG
                                               1979 GCGCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC
                                                                                                                                                                                                                                                                                        1739 AGATGCGCACCGCCCACACCAACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
                                                                                                                                                                                                                                                                                                                                      CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                      AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                3803 TIGICAAIACCCCTCCCTIAGIGAAAITAIGGIACCAGITAGAGAAAGAAAGAAGCCCAIAGIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGA
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Search completed: February 10, 2003, 20:48:31 Job time : 148.195 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 10, 2003, 12:45:48; Search time 107.929 Seconds Run on:

(without alignments) 10843.369 Million cell updates/sec

US-09-610-313-30 2469 Perfect score:

1 gtcgacgccaccatggccga......gggctagcaccggtgaattc 2469 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 408267 seqs, 237001491 residues Searched:

816534

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_NA:*

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//cgn2_6/ptodata/2/pubpna/US6B_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/US6B_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/US6B_UBCOMB.seq:* 11: 12: 13: 9: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | S GOMBINS S | Sequences of | 3-1 Sequence 0, | 1 00 | -7 Segmence 7. | Segment 6 | 11 Segmence 11 | 13 Seguence 13 | Segment 1 | Segment 1 | Segmence 3 | Seguence 4 | o eccentres | V equences | -5 Segmence 5 | -1 Segment 1 | Segmence 56 | | |
|-------------------------------|----------------|--------------|-----------------|---------------|----------------|----------------|----------------|----------------|-----------------|-----------------|----------------|----------------|-----------------|---------------|---------------|---------------|-----------------|--------------|---------|
| Ω | -581-666-60-SD | 1-82-00-8D | US-09-872-73 | US-09-872-733 | US-09-735-487 | US-09-735-487- | US-09-735-487- | US-09-735-487- | US-09-999-183-1 | US-09-737-190A- | US-09-943-286- | US-09-943-286- | US-09-943-286-9 | US-09-798-675 | US-09-798-675 | US-10-097-997 | US-09-886-156-5 | US-09-886-15 | 1 000 |
| DB | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 6 | 6 | თ | c |
| % Query Match Length DB | 4307 | 8366 | 4338 | 2467 | 2601 | 2601 | 2601 | 2601 | 4307 | 9719 | 8933 | 8933 | 8933 | 9544 | 9918 | 2348 | 9793 | 9793 | 0100 |
| % Query Match | 67.2 | 64.5 | 63.1 | 48.2 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 43.7 | 43.7 | 43.7 | 43.5 | 43.5 | 35.2 | 34.7 | 34.7 | |
| Score | 1659.4 | 1592.8 | 1557.4 | 1190.6 | 1132 | 1132 | 1132 | 1132 | 1132 | 1132 | 1079.6 | 1079.6 | 1079.6 | 1073.2 | 1073.2 | 868.8 | 856.2 | 856.2 | 0 2 2 3 |
| Result No. | н | 7 | က | 4 | S | ٥ | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 0 |

ALIGNMENTS

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1086 CCTGCCTGAGCCCATGAGCCAGCTGCCAACTCCGCTACCATCATGATGCAGCGCGGCAA 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 CTTCAAGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 CCGCAACTGCCGCGCCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 GATGAAGGACTGCACGAGGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.2%; Score 1659.4; DB 10; Length 4307; Best Local Similarity 82.4%; Pred. No. 2.4e-266; Matches 1956; Conservative 0; Mismatches 401; Indels 16; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Codon optimised gagpol sequence
US-09-183-2
                                                                              GENERAL INFORMATION:
APPLICANT: MITROPHANOUS, et al
ITILE OF INVENTION: IN VIVO Selection Method
FILE OF INVENTION: IN VIVO SELECTION METHOR OF THING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: PGT/GB0/02136
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: SEQWINS: 26
                                                Sequence 2, Application US/09999183 Patent No. US20020147169A1
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4307
RESULT 1
US-09-999-183-2
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| qq | 1266 GA | GATGAAAGACTGTACTGAGAGACAGGCTAA-TTTTTAGGGAAGATCTGGCCTTCCTACA 1324 |
|----------|---------------------------|---|
| Qy | 249 GGC | SCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAAAAAGCCCCACCAGCCGCĞ |
| g | 1 25 AG | |
| O.Y | 309 GCT(111 | TICCAGGTGCGCGGCGACAACCCCGCAGCGAGCCGCGCGCGAGCGCCAAGG 362 |
| δλ | 63 | CCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAA 41 |
| qq | 1445 AAC | TA. |
| ογ | 17 | |
| QQ | 1505 GA | AGGGGGGCAGCICAAGGAGGCICTCCTGGACACCGGAGCAGACGACACCGTGCTGGA 15 |
| Qy | <u>`</u> | SATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGCGCATCGGCGGCTTCAT 5 |
| QQ | 1565 GG | BATGICGIIGCCAGGCCGCIGGAAGCCGAAGAIGAICGGGGGAAICGGCGGIIICAI 16 |
| Qy | 537 CAJ 1625 CAJ | CAAGGTGCGCCAGTACGACCAGATCGTGATCGAGATCTGCGGCAAGAAGGCCATCGGCAC 596 |
| Qy | 597 CG | CTGGG 65 |
| qq | 1685 CG | GTGGGCCCCACACCCGTCATCATCGGACGCAACCTGTTGACGCAGATC |
| Qγ | 657 CT | CTGCACCCTGAACTICCCCATCAGCCCCATGAGACCGTGCCCGTGAAGCTGAAGCCCGG 716 |
| ФФ | 1745 TT | SCTGAACTICCCCATTAGCCCTATCGAGACGGTACCGGTGAAGCTGAAGCCCG |
| ٥٥ لو | 717 CA | CATGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCTGAC 776 [|
| ò | 77 | GAGGAGATGGAGAAGGAGGCCAAGATCACCAAGATCGGCCCCGAGAACCC 83 |
| qq | 1865 GG | |
| δy | 837 CT | CTACAACACCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGT 896 |
| qq | 1925 GT | GCTGGT 19 |
| δy | 897 GG | GGACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCC 956 |
| Dp | 1985 GG | GGCAT |
| Qy Db | 957 CC 1 2045 GC | CCACCCCGCCGCCGCGTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGGCGACGCCTA 1016 |
| Qy | 1017 CT | TCAGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCAT 1076 |
| Dp | 2105 CT | CITCICCGITCCCCTGGACGAGACTICAGGAAGTACACTGCCTTCACAATCCCTTCGAI 2164 |
| δy | 1077 CAA | ACAACGAGACCCCGGCATCCGCTACAGTACAACGTGCTGCCCCAGGGCTGGAAGGG 1136 |
| QQ | 2165 CA | SAACGAGACACCGGGGATTCGATATCAGTACAACGTGCTGCTCCCCAGGGCTGGAAAG |
| δλ | 137 | CCCCAGCATCTTCCAGAGCAGCATCACCAAGATCCTGGAGCCCTTCCGCGCCCGCAA 119 |
| QC | 2225 CT | CCGCAATCTTCCAGAGTAGCATGACCAAAATCCTGGAGCCTTTCCGCAAACAGAA 228 |
| Qy Dp | 1197 CC | CCCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCGGGGAT 1256 |
| οy | 57 C | SCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGGCTT |
| Db | 1 2345 AG | |

2216 2276 1556 1616 1736 1796 1856 2944 1916 1976 2036 3124 2096 3244 3304 3364 3424 1436 1496 1376 CGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGA 1676 2764 2824 3004 2524 2584 2704 GGGCGCCGAAACCTTCTACGTGGATGGGGCCGCTAACAGGGAGACTAAAGCTGGGCAAAAGC CGAGCTGGTGAACCAGATCATCGAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTG GGTGCCCCCCCACAAGGGCATCGGCGCCAACGAGCAGATCGACAAGCTGGTGAGCAAGGG GAAGACCGAGCTGCAGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACAT CGTGACCGACAGCCCAGGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAG CACCCCCACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCA 2405 CACACCCGACAAGAAGCACCAGAAGGAGCCTCCCTTCCTCTGGATGGGTTACGAGCTGCA 2465 CCCTGACAAATGGACCGTGCAGCTATCGTGCTGCCAGAGAAAAAAAGACAGCTGTCAA 2585 GGTGAGGCAGCTGTGCGAAACTCCTCCGCGGAACCAAGGCACTCACAGAGGTGATCCCCCT CGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAA 2885 CACCACCGAAAGCATCGTGATCTGGGGAAAGACTCCTAAGTTCAAGCTGCCCATCCAGAA GGAGACCTGGGAGCCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGA GTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCAT CGGCGCCGAGACCTTCTACGTGGACGCCGCCCAACCGCGAGACCAAGATCGGCAAGGC CCCCGACAAGIGGACCGIGCAGCCCAICGAGCIGCCCGAGAAGGAGGAGCIGGACGTGAA 2525 CGACATACAGAAGCTGGTGGGGAAGTTGAACTGGGCCAGTCAGATTTACCCAGGGATTAA GGTGCGCCAGCTGTGCAAGCTGCTGCGGGGGCGCCAAGGCCCTGACCGACATCGTGCCCCT GACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCA CCAGIGGACCIACCAGAICIACCAGGAGCCCTICAAGAACCIGAAGACCGGCAAGIACGC CATCCGCAAGGTGCTGTTCCTGGACGGCATCGA 2369 1857 1977 3245 2217 2277 1497 1557 1617 2705 1677 2765 1737 2825 1797 2945 1917 3008 3065 2037 3125 2097 3185 2157 3305 3365 2337 1317 1377 g qq q δŷ Db Qγ Pp δy qq ŏλ g $^{\circ}$ qq οy qq δy ρp QΥ Dp δ 임 QΥ δy g g Qγ Pb δ qq QΥ qq δy οy QY

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Page

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APPLICANT: The Government of the United States of America, as TITLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND TITLE OF INVENTION: SIV ENV GENES
FILE REFERENCE: 2026-42870S1 HIV GAG/POL,SIV GAG & ENV CURRENT APPLICATION NUMBER: 05/09/872,733
CURRENT FILING DATE: 2001-66-01
PRIOR FILING DATE: 2000-1-2-2
PRIOR FILING DATE: 2000-1-2-2
PRIOR FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2037 TGAAAGATTGTACTGAGAGACAGGCTAA-TTTTTAGGGAAGATCTGGCCTTCCTACAAG 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2216 CIGIAICCITIAACIICCCICAGAICACICITIGGCAACGACCCCICGICACAGIAAGGA 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGGGGGGCAACTCAAGGAAGCGCTGCTCGATACAGGAGCAGATGATACAGTATTAGAAG 2335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAACTGCCGCCCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCCAAGGAGGGCCCACCAGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAGGACTGCACCGAGCGCCAAGCTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAGGTGCGCGG-----CGACAACCCCCGCAGCGAGGCCGGCCGAGCGCCAAGGCCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description of Artificial Sequence: DNA sequence;
CTHER INFORMATION: of the construct pCMVgagpolBnKan containing a CMV OTHER INFORMATION: promoter, a HIV gag/pol gene and a kanamycin US-09-872-733-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCCGACGACGTGCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGTGCGCCAGTACGACCAGATCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1592.8; DB 10; Length 8366;
Pred. No. 2.5e-255;
0; Mismatches 442; Indels 16;
                   Sequence 6, Application US/09872733
Patent No. US20010036655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.58; 8
80.78; I
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.7 Matches 1914; Conservative
                                                     GENERAL INFORMATION:
APPLICANT: The Gove
US-09-872-733-6
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                     2576 TGGACGCCCCAAGGTCAAGCAATGGCCATTGACGAAAGAGAAGATCAAGGCCTTAGTCG
                                                                                                                                                                                                                            2696 ACAACACTCCAGTCTTCGCAATCAAGAAGAAGAAGATACCAAGTGGAGAAAGCTGGTGG
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TGCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT
                                                                     GCACCCTGAACTTCCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
                                                                                                                                      719 TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG
                                                                                                                                                                                                        779 CCATCTGCGAGGAGATGGAGAAGGAGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT
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Sequence 1, Application US/09872733

Patent No. US20010036655A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as

TITLE OF INVENTION:

PRIOR APPLICATION NUMBER: US/09/872,733

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/173,036

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 19
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                                                            1739 AGATGCGCCACGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG 1798
                                                                                                                                                    CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1858
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3536 AATGGACCTACCAATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGCAAGTACGCAA
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                                                                                     1919 TCGTGAACACCCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG
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                                                        191 TGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG
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  DB 10; Length 4338;
                            0; Mismatches 441; Indels
Score 1557.4; DB 1 Pred. No. 1.7e-249;
 63.1%;
80.5%;
                            Matches 1914; Conservative
                Best Local Similarity
    Query Match
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                                                                                            GGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCCGC 1194
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FILE REFERENCE: 2026-4287081 HIV GAG/POL, SIV GAG & ENV CURRENT APPLICATION NUMBER: US/09/872,733

CURRENT APPLICATION NUMBER: US/09/872,733

CURRENT FILING DATE: 2001-06-01

PRIOR PILLING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/173,036

PRIOR FILLING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PATENTIN VEY. 2.1

SEQ ID NO 3.1
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; Patent No. US20010036655A1
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                  1210 ATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCACCGC
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Sequence 7, Application US/09735487

Batent No. US20020042679A1

GENERAL INFORMATION:

APPLICANT: GE BETHUNE, Marie-Pierre

APPLICANT: HERDGS, Kurt

APPLICANT: PAUWELS, Rudi

TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY

TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY

TITLE OF INVENTION: OF HUMAN HIV STRAINS

FILE REPRENEUR: 1377-125P

CURRENT APPLICATION NUMBER: US/09/735,487
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tive 0; Mismatches 730;
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PRIOR APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
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METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY OF HUMAN HIV STRAINS

APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: HERTOGS, Kurt
APPLICANT: HEAVWELS, Rudi
TITLE OF INVENTION: METHOD OF MANAGING THE
TITLE OF INVENTION: HIV POSTITIVE BASED ON
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/735,487

Sequence 9, Application US/09735487 Patent No. US20020042679A1 GENERAL INFORMATION:

US-09-735-487-9

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                                                                                                                                                                                                                          45.8%; Score 1132; DB 10; 68.5%; Pred. No. 3.4e-179;
                                                                                                                                                                                                                                                       0; Mismatches 730;
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 2601
                                                                                                                                               NAME/KEY: CDS
LOCATION: (334)..(489)
OTHER INFORMATION: gag P6 (52 AA)
                                                                                                                                                                                                                                     Best_Local Similarity 68.59 Matches 1626; Conservative
                                                                                                                    ORGANISM: HIV-HXB2
                                                                                                                                                                                             09-735-487-9
                                                                                                        TYPE: DNA
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                                                 899 ACTTCCGCGGAGCTGAACAAGCGCACCCAGGACTTCTGGGGAGGTGCAGCTGGGCATCCCCC
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APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: HERNOGS, Kurt
APPLICANT: HERNOGS, Kurt
APPLICANT: HERNOGS, Kurt
APPLICANT: PAUWELS, Rud
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: OF HUMAN HIV STRAINS
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-1259
CURRENT APPLICATION NUMBER: US/09/735,487
CURRENT APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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68.5%; Pred. No. 3.4e-179;
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Patent No. US20020042679A1
GENERAL INFORMATION:
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OTHER INFORMATION: Protease
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Matches 1626; Conservative
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ORGANISM: HIV-HXB2
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TYPE: DNA ORGANISM: HIV-HXB2
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1199 CCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCG 1258
                                1336 GGCAGCATAGAACAAAAATAGAGGAGCTGAGACAACATCTGTTGAGGTGGGGACTTACCA 1395
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APPLICANT: PAUWELS, Rudi
TITLE OF INVEWTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVEWTION: HIV DOSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVEWTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/735,487
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
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                      2356 TACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAA 2415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 GCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGA 190
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Indels
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                                                                                                                                    2416 TCAGGAAAGTACTATTTTAGATGGAATAGAT 2447
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; OTHER INFORMATION: Reverse Transcriptase
US-09-735-487-13
                                                                                 2339 TCCGCAAGGTGCTGTTCCTGGACGCCATCGAT
                                                                                                                                                                                                                                                                                                                                                        de BETHUNE, Marie-Pierre
                                                                                                                                                                                                                                                                   Sequence 13, Application US/09735487
Patent No. US20020042679A1
GENERAL INFORMATION:
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Matches 1626; Conservative
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PAUWELS, Rudi
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SOFTWARE: PatentIn Ve
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| ζ, q | 599 | TGCTGATCGGCCCACCCCGGGAACATCGGCCGCAACATGCTGACCAGGTGGGCT 658 | |
| 7.7 Op | 659 | GCACCCTGAACTICCCCATCAGCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA 718 | |
| 7 <u>7</u> | 719 | TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 778 | |
| 37 28 | 977 | CCATCTGCGAGGAGGATGGAAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT 838 | |
| 7. Q0 | 839 916 | ACAACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCACGTGGCGCAAGCTGGTGG 898 | |
| 57 27 | 936 | ACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC 958 | |
| 27 27 | 959 1036 | ACCCGCCGGCCTGAAGAAGAAGAGGGGGCGCGCGGCGGGCG | |
| λ q | 1019 | TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 1078 | |
| 2 <u>y</u> | 1079 | ACAACGAGACCCCCGGCATCCGCTACCAGTACACGTGCTGCCCCAGGGCTGGAAGGGCA 1138 | |
| 2y 0b | 1139 | GCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCGCAACC 1198 | |
| 2y 2b | 1199 | CCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCGACCTGGAGATCG 1258 | |
| λχ Op | 1259 | GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCACCTGCTGCGCTGGGGCTTCACCA 1318 | |
| 2y 0b | 1319 | CCCCGGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC 1378 | |
| . Y2 dc | 1379 | CCGACAAGTGGACCGTGCACCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACG 1438 | |
| 7. Op | 1439 | ACATCCAGAAGCTGGTGGCCAGCTGAACTGGGCCAGCCAG | |
| 7.7 Q0 | 1499 1576 | TGGGCGAGCTGTGCAAGCTGCTGCGGGGGCCCAGAGGCCCTGACCGACATCGTGCCCCTGA 1558 | |
| 27 | | 161 | |

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                                                                                                                      2279 TGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCA 2338
1636 CAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATTCTAAAAGAACCAGTACATG 1695
                                                                                                   1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1738
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                                                   1696 GAGTGTATTATGACCCATCAAAAGACTTAATAGCAGAAAATACAGAAGAGGGGCAAGGCC
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Patent No. US20020147169A1

GENERAL INPORMATION:
APPLICAMT: MITROPHANOUS, et al
TITLE OF INVENTION: In Vivo Selection Method
FILE REFERENCE: 674523-2009
CURRENT EDILATION NUMBER: US/09/999,183
CURRENT FILING DATE: 2001-11-29
PRIOR PILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: PCT/GB00/02136

PRIOR PILING DATE: 1999-06

NUMBER OF SEQ ID NOS: 26

SOFTWARE: SEQWIN99

SEQ ID NO 1

LENGTH: 4307
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                                                                                      2467 CTGATAAATGGACAGTACACCTATAGTGCTGCCAGAAAAAGACAGCTGGACTGTCAATG
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                                                                           1079 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA
                                                                                                                     CACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAAATC
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APPLICANT: Shibuya, Tetsuo
TITLE OF INVENTION: A Method for Changing a Target Array, a Method for Analyzing
TITLE OF INVENTION: A Structure, and an Apparatus, a Storage Medium and a
TITLE OF INVENTION: Transmission Medium Therefor
FILE REPERENCE: 999199990270031 (14043)
CURRENT APPLICATION NUMBER: US/09/737,190A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 1
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 GATATGTTACTAATAGAGGAAGACAAAAGTTGTCACCCTAACTGACACAACAAATCAGA 3186
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                        2099 AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCGAGGTGAACATCG
                                          3247 TAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAACCAGATCAAAGTGAATCAG
                                                                                                                                                                                 TGCCCGCCCACAAGGGCATCGCCGCCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCA
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                                                                             TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCG
                                                                                                                               ACCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG
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68.5%; Pred. No. 3.6e-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Human iImmunodeficiency virus type 1
                                                                                                                                                                                                                                     2339 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
                                                                                                                                                                                                                                                    Sequence 1, Application US/09737190A Patent No. US20020102545A1
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US-09-737-190A-1
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                                                    419 TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGCTGCTGGAGG
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1679 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA
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TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02.UT
CURRENT APPLICATION NUMBER: US/09/943,286
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                              Query Match
43.7%; Score 1079.6; DB 1
Best Local Similarity 55.7%; Pred. No. 1.7e-170;
Matches 1341; Conservative 281; Mismatches 734;
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                             Virus
                                            TYPE: RNA
ORGANISM: Human Immunodeficiency
                                                                                                     LOCATION: (1)...(8933)
OTHER INFORMATION: Sequence
COTHER INFORMATION: plasmid.
US-09-943-286-3
                                                                         FEATURE:
NAME/KEY: source
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3119 AGUAUUGGCAAGCCACCUGGAUUCCUGAGUGGGAGUUUGUUAAUACCCCUCCUUUAGUGA 3178
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: LOCATION: (4135)...(4155)

: OTHER INFORMATION: Mutated positions: 4135, 4140-1, 4145, 4150,

: US-09-943-286-4
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; Patent No. US20020106668A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (4140)...(4159)
; OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152,
US-09-943-286-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Sequence of the IAC-Bscr pseudo target
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD FILE REFRENCE: 6P104-02.UT CURRENT APPLICATION NUMBER: US/09/943,286 CURRENT FILING DATE: 2001-08-30 NUMBER OF SEQ ID NOS: 9 SOFTWARE: FeatSEQ for Windows Version 3.0 SEQ ID NO 9
                                                                                                                                                                                                           Sequence 9, Application US/09943286 Patent No. US20020106668A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA ORGANISM: Artificial Sequence
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                                                                         2363 GCATCGAT 2370
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US-09-943-286-9
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2819 CAGAAAACAGAGAGAUUCUAAAAGAACCAGUACAUGGAGUGUAUUAUGACCCAUCAAAAG 2878
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                                                            2939 AGCCAUUUAAAAAUCUGAAAAAAGAGGAAAAAUGAGGGAAGAAUGAGGGGUGCCCACACUAAUG
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TITLE OF INVENTION: HIV VACCINES
FILE REFERENCE: E056 2020
CURRENT APPLICATION NUMBER: US/09/798,675
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR FILING DATE: 2000-03-02
PRIOR PPLICATION NUMBER: US 60/251,083
PRIOR FILING DATE: 2000-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09798675 Patent No. US20020106798Al GENERAL INFORMATION:
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SOFTWARE: PatentIn versic
SEQ ID NO 4
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3599 GAAUAGAU 3606
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OTHER INFORMATION: Construct of vaccine vector pGA2 and insert JS2 expressing cla
                                                                                                                                 LOCATION: (1401)..(3617)
OTHER INFORMATION: encoding viral rproteins including reverse transcriptase
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                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                               Rev regulating transfer of RNA to
                                                                                                                                                                                                                                                                                                                                                                                                           .9e-169;
ss 738; Indels
                                                                                                                                                                                                high level of virus particles
                                                                              LOCATION: (106)..(1641)
OTHER INFORMATION: encoding inner core protein
                                                                                                                                                                                                                                                                                                                                                                                          Score 1073.2;
Pred. No. 1.9e-
0; Mismatches
                                                                                                                                                                                                                                                                            LOCATION: (4102)..(6660)
OTHER INFORMATION: encoding ADA Env NAME/FER: misc-feature
LOCATION: (6672)..(5544)
OTHER INFORMATION: Vaccine vector pGA2
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.5%;
Best Local Similarity 67.2%;
Matches 1618; Conservative
                                                                                                                                                                                                                         OTHER INFORMATION: encodes:
NAME/KEY: misc_feature
LOCATION: (4102)..(6660)
                                                 INFORMATION: HIV-1 VL
                                                                                                                                                                               LOCATION: (3708)..(6334)
OTHER INFORMATION: induces
                                                                  NAME/KEY: misc_feature
                                                                                                                NAME/KEY: misc_feature
LOCATION: (1401)..(3617
                                                                                                                                                                                                               NAME/KEY: misc-feature LOCATION: (3847)..(6518
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| ACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCATCAGCC 682 | CCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGCATGGACGGCCCCAAGGTGAAGCAGT 742 1 1 1 1 1 1 1 1 1 1 | GGCCCCTGACCGAGGAGAATCAAGGCCCTGACCGCCATCTGCGAGGAGAGAGA | AGGGCAAGATCACCAAGATCGCCCCGAGAACCCCTACAACACCCCGTGTTCGCCATCA 862 1 1 1 1 1 1 1 1 1 1 | AGAAGAACACACCAACTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCA 922 | CCCAGGACTICIGGAAGGIGCAGCIGGGCAICCCCCCCCGCCGCCGGCGIGAAGAAGAAGA 982 11 | AGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACT 1042 | TCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGCCCCCGGCATCCGCT 1102 | ACCAGTACAACGTGCTGCCCCAGGCTGGAAGGCCACCCCCGGCATCCTTCCAGAGCAGCA 1162 1 | GACCAAGATCCTGGAGCCCTTCCGCGCGCGCACCCGAGATCGTGATCTACCAGTACA 1222 | GGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCACGCGCGAGATCGAGG 1282 1111 | AGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACCCCGGAAAGAGAGCACCAGAAGG 1342 | AGCCCCCCTTCCTGTGGATGGCTACGAGCTGCACACGACAAGTGGACCGTGCAGCCA 1402 | TCGAGCTGCCCGAGAAGGACAGCTGGAACCGTGAATCCAGAAGCTGGTGGGCAAGC 1462 | TGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGC 1522 | GCGGCGCCAAGGCCCTGACCGACCAATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTGG 1582 11 | CCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTACTACGACCCCAGCAAGG 1642 | ACCTGGTGGCCGAGATCCAGAAGGGCGACGACGAGGGACCTACCAGATCTACCAGG 1702 |
|---|--|---|---|--|---|---|--|--|--|--|---|--|---|---|--|--|---|
| ACATCATCGGCCGCAACATGCT ACATAATTGGAAGAAATCTGTT | CCATCGAGACCGTGCCGTGAA(| GGCCCCTGACCGAGGAGAAGAT(| AGGCAAGATCACCAAGATCGG(AGGGAAAATTTCAAAAATTGG(| AGAAGAAGGACAGCACCAAGTG(| CCCAGGACTTCTGGGAGGTGCAK | AGAGCGTGACCGTGCTGGACGTC | TCCGCAAGTACACCGCCTTCACC | ACCAGTACAACGTGCTGCCCCAC | TGACCAAGATCCTGGAGCCCTTC | TGGACGACCTGTACGTGGGCAGC | AGCTGCGCAAGCACCTGCTGCGC | AGCCCCCCTTCCTGTGGATGGGC | TCGAGCTGCCCGAGAAGGAGGAGC | TGAACTGGGCCAGCCAGATCTAC TGAATACCGCAAGTCAGATTTAC | GCGCCCCAAGGCCCTGACCGAC GAGGACCAAGCACTAACAGAA | CCGAGAACCGCGAGATCCTGCGC | ACCTGGTGGCCGAGATCCAGAAG |
| 623 1852 | 683 | 743 | 803 | 863 | 923 | 983 | 1043 | 1103 | 1163 | 1223 | 1283 | 1343 | 1403 | 1463 2692 | 1523 2752 | 1583 | 1643 |
| Qy Db | Qy Dp | Qy Db | QY Db | QY Db | Qy Db | QY | Qy Db | Qy Db | Qy | Qy | Qy | Qy Dp | QY Db | Oy Dp | Qy Db | Qy | Qy Db |

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2932 AGCCATTTAAAAATCTGAAAACAGGAAAATATGCAAGAATGAGGGGTGCCCACACTAATG 2991
                                                          ACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGG 1822
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AGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCACACCAACG 1762
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APPLICANT: EMCTY University
TITLE OF INVENTION: HIV VACCINES
FILE REFERENCE: E056 2020
CURRENT APPLICATION NUMBER: US/09/798,675
CURRENT APPLICATION NUMBER: US 60/186,364
PRIOR APPLICATION NUMBER: US 60/251,083
PRIOR FILING DATE: 2000-01-01
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 9918
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FEATURE:
TOTHER INFORMATION: Construct of vaccine vector pGAl and vaccine insert expressing OTHER INFORMATION: ade B HIV-1 Gag-Po
NAME/KEY: misc_feature

us-09-610-313-30.rnpb

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Page

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NAME/KEY: misc_feature
LOCATION: (3708)..(5715)
OTHER INFORMATION: regulates high-level production of HIV genes
NAME/KEY: misc_featre
LOCATION: (3847)...(5944)
OTHER INFORMATION: encodes protein regulating the transfer of RNA to cytoplasm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 TGCTGGACACCGGCGCCGACGACGACGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGA
                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (3939)..(4181)
CHER INFORMATION: gene participates in viral assembly and budding
NAME/KEY: misc_feature
LOCATION: (4099)..(4941)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.5%; Score 1073.2; DB 10; Length 9918; 67.2%; Pred. No. 1.9e-169;
                                                                                                                                                                                                                                                                                                                                          LOCATION: (4099)...(4941)
OTHER INFORMATION: encodes truncated form of viral coat protein NAME/KEY: misc.feature
LOCATION: (6098)..(9918)
OTHER INFORMATION: vaccine vector pGA1
                                         NAME/KEY: misc_feature
LOCATION: (1401)..(3617)
OTHER INFORMATION: encodes viral proteins but not integrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 738; Indels
LOCATION: (106)...(1641)
OTHER INFORMATION: encodes proteins of viral inner core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 67.29
Matches 1618; Conservative
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                     1972 GGCCATTGACAGAAGAAAAATAAAAGCATTAGTAGAAATTTGTACAGAAATGGAAAAGG 2031
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CCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGT 742
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                                                                                                                                                   803 AGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCA
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                                                                           GGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGG
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1763 ACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGG 1822
                                     1823 GCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCG 1882
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            2992 ATGTAAAACAATTAACAGAGGCAGTGCAAAAAAAAAACCACAGAAAAGCATAGTAATATGGG 3051
                                                 AGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGCCGCCGAGACCTTCTACGTGGACG 2002
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                                                                                                                            3352 IAGCTITGCAGGATTAGAAGTAAAACATAGTAACACACACACAATATGCATTAG 3411
                                                                                                                                                                                                                                                                      GCATCATCCAGGCCCAGCCCGACAAGAGCGAGCGAGCTGGTGAACCAGATCATCGAGC 2242
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Search completed: February 10, 2003, 21:10:57 Job time: 153.929 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: February 10, 2003, 10:53:38; Search time 6249 Seconds

(without alignments)

11470.669 Million cell updates/sec

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1 4703 Sequence: 2463

Sequence: 1 9tcgacgccaccatggccga......gggctagcaccggtgaattc 2463

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database: GenEmbl:*

GenEmbl:*

1: 9D_ba:*

2: 9D_htg:*

4: 9D_ptg:*

5: 9D_ov:*

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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | due | AA433314 AX455916 | 016254XA | AX427936 | AX427931 | AX427926 | AX427925 | AX427927 | AX427938 | AX427933 | AX427928 | AX427935 | AA42/934 AX427032 | | AF287353 | AX455946 | AX455987 Sequence | AX457088 | AX306428 | AX306429 | AX455954 | AX455952 | AX427923 Sequence | AK 27 937 Secuence | AX019132 | AX035453 | AX056836 | AX283597 | | AX035464 | AX035463 | AX283584 | 006CC#WW | AX180752 | AX180747 | AX306430 | AX149648 Sequence | AF110975 H | ALIGNMENTS | | | 2463 bp DNA linear PAT 06-JUL-2002 WO0204493. | | | | | W., Engelbrecht, S | antigenic hiv type c polypeptides, |
|-----------|---------------|-----------------|------------|----------------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------------------|--------|----------|----------|-------------------|----------|----------|----------|----------|----------|-------------------|--------------------|----------|----------|----------|----------|--------------|----------|----------|----------|----------|----------|----------|----------|-------------------|------------|------------|----------|----------|--|-----------|----------|-----------------|-----------------|----------------------|------------------------------------|
| | DB ID | | 6 A | A | 9 9 | 6 A) | 6 A | 6 A | 6 A | 6 A) | 6 AX | 9 9 | 9 Y | o y | 9 | 6 AX | 12 A | 9 AX | 12 A | 6 AX | 6 AX | 9 YX | 9 Y | 9 Y | 12 AX | 6 AX | 9 AX | 6 AX | 9 AX | 0 AX | 9 Y X | 6 AX | 6 AX | o A A | 9 AX | 6 AX | 9 YX | 9 YX | 6 AX | 14 A | | | | Patent | , , | / 14 900 | <u>.</u> ; | e S | nett, | encoding |
| | Length | 1 1 1 1 1 1 1 1 | 2463 | 2457 | 9166 | 9788 | 9169 | 9194 | ٠, | 12411 | 9785 | 9167 | 9170 | 28/8 | 9792 | 9189 | 4353 | 3015 | 4352 | 2577 | 4343 | 4341 | 1977 | 1965 | 3024 | 9407 | 4307 | 4307 | 4307 | 4307 | 4327 | 4353 | 4642 | 1680 | 1668 | 8366 | 4338 | 3981 | 9010 | 9010 | | | | from F | | 777:19 | construct | sednence | J., Bar | ides en |
| | 거석 | | 100.0 | 6.86 | 82.3 | 82.0 | 81.4 | 81.3 | 81.2 | 81.2 | 81.1 | 80.9 | 6.08 | n 0 | 80.9 | 80.9 | 80.7 | 80.T | 78.4 | 76.6 | 76.3 | 76.1 | 75.7 | 4.07 | 73.6 | 72.4 | 67.1 | 66.3 | 66.3 | 0.0 | 66.0 | 0.99 | 0.0 | 64.2 | 64.0 | 9.69 | 62.1 | 97.0 | 52.8 | 51.0 | | | | 5915 ence 31 | 5915 | 1.0160 | synthetic const | ficial | Megede, | nucleot |
| | Score | | 2463 | 2436.2 | 2027.6 | 2019.2 | 2005.2 | 2001.8 | 2000.2 | 2000.2 | 1996.8 | 1993.4 | 1993.4 | 1993.4 | 1993.4 | 1991.8 | 1988.8 | 1972.2 | 1932 | 1886.6 | 1879 | 1875 | 1865.4 | 1857.8 | 1798.8 | 1784 | 1651.8 | 1632.6 | 1632.6 | 1624 6 | 1624.6 | 1624.6 | 1624.6 | 1581.2 | 1575.2 | 1566 | 1530.6 | 7.8151 | 1255.8 | 1255.8 | | | | AX45 Sequ | AX45 | . WA4. | Σ | | -1 -50 | |
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                                  zur Megede, J., Barnett, S.W., Engelbrecht, S. and van Rensbu
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Patent: WO 0204493-A 30 17-3AN-2002;
CHIRON CORPORATION (US); University of Stellenbosch (ZA)
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| Qy Db | 601 | CTGATCGGCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGC 60 | |
| Qy | 661 | ACCCTGAACTICCCCATCAGCCCCATCGAGACCGTGCAGGGGAAGCTGGAGCTGG 720 | |
| Qy Db | 721 | GACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC 780 | |
| Qy | 781 | ATCTGCGAGGAGATGGAGAGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC 840 | , |
| Oy Db | 841 | AACACCCCGTGTTCGCCATCAAGAAGAAGGCGCACCAAGTGGGGGAAGCTGGTGGAC 900 | |
| QY | 901 | TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC 960 | |
| QY Db | 961 | CCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGCGGCGACGCCTACTTC 1020 | |
| QY | 1021 | AGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCCAGCATCAAC 1080 | |
| QY Db | 1081 | AACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC 1140 | |
| Qy Db | 1141 | CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGGGCCCGCAACCCC 1200 | |
| Qy Db | 1201 | GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAC 1260 | |
| Qy Db | 1261 | CGCGCCAAGATCGAGGACTGCGCAAGCACCTGCTGCGGTGGGGCTTCACCACCCCCGAC 1320 | |
| Qy Dp | 1321 | AAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGACTACGAGCTGCACCCCGACAAG 1380 | |
| Qy Db | 1381 | TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGAGAGCTGGACCGTGAACGACATCCAG 1440 | |
| Qy | 1441 | AAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAG 1500 | |
| Qy Dp | 1501 | CTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGG 1560 | |
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/db_xref="taxon:32630"
/db_*plasmid pWR1012x/s containing HIV genes"
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                          Huang, Y. and Nabel, G.J.
Modifications of hiv env, gag, and pol-
genetic immunication
Patent: WO 0232943-A 168 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
1.9166
         artificial sequences
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Pred. No. 4.1e-203;
); Mismatches 178;
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/db_xref="taxon:32630"
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Patent: WO 0232943-A 174 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="plasmid pVR1012x/s containing
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Modifications of hiv env, gag, and pol
genetic immunization
Patent: WO 0232943-A 169 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
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81.4%; Score 2005.2;
Best Local Similarity 91.4%; Pred. No. 1.2e
Matches 2187; Conservative 0; Mismatches
                                                                                                                       Sequence 169 from Patent W00232943. AX427931
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TGATCGGCCCCACCCCCGTGAACATCATCGCCCGCAACATGCTGACCCAGCTGGGCTGCA
                                                                CCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG
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Modifications of hiv env, gag, and pol-
genetic immunization
Patent: WO 0232943-A 164 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0232943-A 163 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
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                                          1553 CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG
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   enhance immunogenicity
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                                                                                                                           /note="plasmid pVR1012x/s containing HIV genes" 3733 c 3476 g 2264 t
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                                                                                                                                                                                              Score 2000.2; DB 6;
Pred. No. 3.8e-201;
0; Mismatches 188;
                                                                                               /organism="synthetic construct"
/db_xref="taxon:32630"
Modifications of hiv env, gag, and pol
             genetic immunization
Patent: WO 0232943-4 165 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
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Best Local Similarity 91.2%;
Matches 2185; Conservative
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| | GCCCGAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGGCCCGCCGCCCGC | 346 CGGACAAGTGGAACCGTGCCGAGAAGGGAGGTGGACGGAGGGAG | CGTGTACTACGACCCCAGGAAGGACCTGATCGCCGAGATCCAGAAGCAGGCCCGGGCCCGTGGAACCTACCAGAAGCAGGCCCAGGGCCCGTGGAACCTACCAGAAGCAGGCCCAGGGCCCGTGGAACCTACCAGAAGCAGGCCCCAGGGCCCAGTCCACAACTCAAGAACCTGAAGACCTGCAGAAGTACGCCCAGTTCAAGAACCTGAAGACCTGAAGACCTGCAGAAGTACGCCCCCAGAACTACCACACACA |
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0232943-A 176 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
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                                1973 GCGCCGAGACCTTCTACGTGGACGCGCCCAACCGCGAGACCAAGATCGGCAAGGCCG 2032
                                                  4946 GCGCCGAGACCTTCTACGTGGACGGCCCCCAACCGCGAGACCAAGGCCG 5005
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2843 c 2731 g 1851 t
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| TAT GCG | CCTTTAGCTTCCCTCAGATCACTCTTTGGCAGCGACCCCTCGTCACTAATAAAGATAG SCCAGATCAAGAGGCCCTGCTGGACACCGGCGCCGACGACACGTGCTGGAGGAA | m & . |
| 3 5 2 | GGCCASCTGAAGGAGGCCCTTCTAGACACCGGCGCGCGACGACGACGGTGGTTGGGGGAAAAAGCTGGCGGGCAAGATGATGGCGGGGGGGG | 41 49 |
| ě-ē | AGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAGGCC | .01 .557 |
| $\vdash - \vdash$ | GATGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCA 6 | 61 |
| $\circ - \circ$ | CCTGAACTTCCCCATCGCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG 7 | 21 |
| A A | ACGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCA 7 | 81 1737 |
| \vdash $ \vdash$ | CTGCGAGGAGATGGAGAGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACA (| 841 3797 |
| a – a | ACACCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGACT S | 901 3857 |
| ₽ ₽ | CCGCGAGCTGAACAAGGGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACC | 961 3917 |
| 0-0 | CCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTCA 1 | 1021 3977 |
| 0 0 | GCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACA 1 | 1081 4037 |
| | ACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCC | 1141 |
| • | CCAGCATCITCCAGAGCAGCATGACCAGATCCTGGAGCCCTTCCGCGCCCGCACCCCG | 1201 4157 |
| ~ ~ | AGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCC 3 | 1255 |
| a – a | AGCACCGGGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCTGGGGCTTCACCACC : | 1315 4277 |

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CCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCG
         TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA
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                                    ACAAGTGGACCGTGCCGATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACGACA
                                                                       TCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGC
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Pred. No. 2.1e-200;
0; Mismatches 186; Indels 27;
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2668 c 2517 g 1757 t
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                                                                                                                        Huang, Y. and Nabel, G.J.
Modifications of hiv env, gag, and pol
genetic immunization
Patent: WO 0232943-A 171 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
LOCATION/QUALIFIERS
                        DNA
                                  Sequence 171 from Patent W00232943.
                        9167 bp
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AX427933.1 GI:21538020
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Best Local Similarity 91.1%;
Matches 2182; Conservative C
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0232943-A 166 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
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Score 1993.4; DB 6; Length 9170;
Pred. No. 2.1e-200;
0; Mismatches 186; Indels 27;
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/note="plasmid pvR1012x/s containing
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                                                                                                                                 GCAACTGCCGCCCCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGA
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| ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA GCCCCAGCATCTTCCAGAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCCGCAACC [| CCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC CCCCGACAAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC CCCCGACAAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC CCGACAAGTGGACGCCCCACGAGAGCCCCCTTCTGTGATGGTTACGAGCTGAACG CGACAAGTGGACGTGCAGCCCATCGTGCTGCCCGAGAAGGAAG | CCGAGGAGCCGAGCTGGCCGAGAACCGGGAGATCCTGCGCGGGGCCGTGCACG | AGATGGGCACCCCAACCAACGACGTGAAGGACCTGACCGAGGCCGTGCAGAAGATCG I | GCGCGAGACCTTCTACGTGGCGCCCCACCAACCGCCAACATCAGGCGGGCG |
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                2213 AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG 2272
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Matches 2182; Conservative 0; Mismatches 186;
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| | GGTGGGCCAGTACGACAGATCCTGATCGAGATCTGCGGCCACAAGGCCATCGGCACO GCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGC | GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCGTGAAGCTGAAGCCGGGCA | TGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAATCAAGGCCCTGACCG | CCATCTGCGAGGAGATGGAGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT | ACAACACCCCGGGGTGTTCGCCATCAAGAAGAACACACAACAACAAGGGGGGCAAGCTGGTGG | ACTICCGCGAGCIGAACAAGCGCACCCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCC | ACCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGGGACGCCTACT | TCAGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA | ACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCTGCCCCAGGGCTGGAAGGGCA | GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGGGCCCGCAACC | CCGAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCG | GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA | CCCCGGACAAGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCACCCITIIIIIIIIII | CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACG | ACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCA | TGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGA |
| 3 2 7 | 4113 599 4173 | 659 | 719 | 779 | 839 | 899 | 959 4533 | 1019 | 1079 4653 | 1139 | 1199 | 1253 | 1313 | 1373 | 1433 | 1493 |
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1553 CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGGCCCGTGCACG
                1613 GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC
                                                                       5193 GCGTGTACTACGACCCCAGCAAGGACCTGATCGCCGAGATCCAGAAGCAGGGCCAGGCC
                                                                                                                1673 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA
                                                                                                                              1733 AGATGCGCACCGCCCACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
                                                                                                                                                                                                                                CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGG
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Huang, Y. and Nabel, G.J.
Modifications of hiv env, gag, and poigenetic immunization
Patent: WO 0232943-A 172 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)

AUTHORS TITLE JOURNAL

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                                                                          Score 1993.4; DB 6;
Pred. No. 2.1e-200;
0; Mismatches 186;
Location/Qualifiers
1. .9783
Acyanism="synthetic construct"
db_xref="taxon:32630"
                                      /note="plasmid
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/db_xref="taxon:32630"
/note="plasmid pVR1012x/s containing
a 2898 c 2725 g 1830 t
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Modifications of hiv env, gag, and pol-
genetic immunization
Patent: WO 0232943-A 170 25-APR-2002,
GOVERNMENT OF THE UNITED STATES (US)
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 170 from Patent W00232943.
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| | 373 CCGACAATTGGACCGTCCA 341 CCGACAAGTGGACCGTCCA 433 ACATCCAGAAGCTGGTCGG 401 ACATCCAGAAGCTGGTCGG 493 TGCGCCAGCTGTGCAGCT 6111111111111111111111111111111111111 | 553 CCGAG 521 CCGAG 613 GCGTG 581 GCGTG 673 AGTGG | 33 01 93 61 53 | 13 TCG 81 TCG 73 GCG 71 GCG 41 GCG 33 GCT | 93 AGAC 1111 61 AGAC 53 TGAC 21 TGAC 113 AGCT 11111 81 AGCT 73 TGCC 73 TGCC | 33 TCCGCAAGGTGCTGTTCCJ |

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. 1 2 3 3 4 4 4 7 | Score 2442.2 2442.2 2035.2 2025.2 2019.2 | % Query Match 100.0 99.2 983.3 82.3 82.2 | Query Query Authorized Length DB 63 100.0 2463 24 2 99.2 2467 24 46 83.1 2306 21 6 82.3 9166 24 2 82.2 2312 21 2 82.0 2300 21 | DB 244 21 24 21 22 21 22 21 21 21 21 21 21 21 21 21 | SUMMARIES ID ABL39960 ABL39961 AAA70479 AAA70481 AAA70481 | Description Synthetic construc Synthetic construc Synthetic construc HIV FS()_ProtMod HIV FS() ProtMod HIV FS() ProtMod |
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ALIGNMENTS

RESULT 1

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Human immunodeficiency virus type C; antigenic HIV type C protein;
immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef;
immunostimulant; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                             Zur Megede J, Barnett SW, Engelbrecht S, Van Rensburg EJ;
                                                                          Synthetic construct PR975YM SEQ ID NO:31.
                                                                                                                                        Human immunodeficiency virus type C. Synthetic.
         ABL39960 standard; DNA; 2463 BP
                                                                                                                                                                                                                 05-JUL-2001; 2001WO-US21241.
                                                                                                                                                                                                                                       05-JUL-2000; 2000US-0610313
                                                     (first entry)
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                                                    15-MAY-2002
                                                                                                                                                                                              17-JAN-2002.
                               ABL39960;
ABL39960
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New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy $\,$

Claim 1; Fig 9; 233pp; English.

polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding day, Pol. Vif. Vpr. Tat. Rev. Vpu. Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06226 to ABB06215 represent sequences used in the present invention describes expression cassettes comprising a exemplification of the present invention.

Sequence 2463 BP; 567 A; 835 C; 759 G; 302 T; 0 other;

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540 900 999 GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGGAG 480 ACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG 720 61 CGCAGCAACTICAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGAGGGGC 120 GGCCACCAGATGAAGGACTGCACCGAGCCCAGGCCAACTTCTTCCGCGAGGACCTGGCC 240 AGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCAGCGAGGCCGGCGCGCGAGCGCCAAG 360 AGCCGCGAGCTGCAGGTGCGCGCGACAACCCCCGCAGCGAGGCCGGCGCGAGCGCCAG 360 GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTG 420 CGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC 120 121 CACATCGCCCGCAACTGCCGCGCCCCCCGCAAGAAGGCCTGCTGGAAGTGCGGCAAGGAG 180 0; Gaps 1 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG 60 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGAGCCATCGGCACGTG 481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGCATCGGCGGCGTTCATCAAG 541 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCAAGAAGGCCATCGGCACCGTG CTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGC 601 CTGATCGGCCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGC TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACC 481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGATCGGCGCGTTCATCAAG 661 ACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG 1 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCCAACATGCTGATGCAG Query Match 100.0%; Score 2463; DB 24; Length 2463; Best Local Similarity 100.0%; Pred. No. 1.4e-300; Matches 2463; Conservative 0; Mismatches 0; Indels 0; Query Match 661 541 601 181 181 241 241 301 301 361 361 421 421 q οy рp δ g Ω g oγ q φý g ò g a g ò g δy ŏ g òγ Qγ οy ò

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AGCATCGTGATCTGGGGCAAGACCCCAAGTTCCGCCTGCCCATCCAGAAGGACCCTGG 1860 1681 TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGCAAGTACGCCAAGATGGGC 1740 1440 1621 TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACC 1680 1681 TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC 1740 1741 ACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG 1800 1501 crergcaagcrecrecegeeeceaageccreaceacarcarcerecereacegagag 1560 1561 GCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCCGTGCACGGCGTGTAC 1620 AGCGTGCCCCTGGACGACGTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC 1080 1021 AGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC 1080 1141 CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCC 1200 1441 AAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAG 1500 1081 AACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC 1140 961 CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTC 1020 1321 AAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGTGCTGCACCAGACAAG TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACGACATCCAG 1441 AAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAG 1561 GCCGAGCTGGCCGAGACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTAC 1621 TACGACCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGCCACGACCAGTGGACC 1501 CTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAG 1081 AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCCCCCAGGGCTGGAAGGCAGG 1201 GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGGACCTGGAGATCGGCCAGCAC 841 AACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGAC 901 TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC 961 CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCTGGACGTGGGCGACGCCTACTTC ATCTGCGAGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC 781 ATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC 841 AACACCCCCTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGAC 1801 1021 1381 781 q g g δy 셤 δ g QQ Ωp δX g QΫ g δλ ò δλ QQ g g ά 셤 ò ÓΫ δλ g ò ŏ ŏ δλ a ò g ò

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Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds.
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                      GAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1920
                                                                  ACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAG 1980
                                                                            AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAGAGGTGTACCTGAGCTGGGTGCCCGCC 2280
                                                                                                                                                                                                                                                                                                                                                                                             1801 AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG 1860
                                                                                                                                                                                                   CTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGAC 2160
                                                                                                                                                                                                                                               CACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAG 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                              TACGTGGGCAGCGCCCCCTAGGATCGATTAAAAGCTTCCCGGGGGCTAGCACCGGTGAA 2460
                                  ACCTTCTACGTGGACGGCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG
                                                                                                                                   ACCTTCTACGTGGACGCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG
                                                                                                                                                        Synthetic construct PR975(+) SEQ ID NO:30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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TTC 2463
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The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06215 represent sequences used in the exemplification of the present invention.
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                                                                                        New polynucleotides encoding antigenic HIV Type C polypeptides, usefuin applications including DNA immunization or generation of packaging
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121 CACATCGCCGGCAACTGCCGCGCCCCCCCAAGAAGGCTGCTGGAAGTGCGGCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGGCCACCAGGGCCAACCATCCTGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATGCTGATGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24; Length 2469;
                                 EJ;
                                 Van Rensburg
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                               Sequence 2469 BP; 571 A; 833 C; 761 G; 304 T; 0 other;
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.:
                                                                                                                                                                                                                                                                                                                                                                                             99.2%; Score 2442.2; DB 2.
99.6%; Pred. No. 5.6e-298;
Live 0; Mismatches 3;
                               Engelbrecht S,
                                                                                                                      cell lines, particularly in gene therapy
                                                                                                                                                 Claim 1; Fig 8; 233pp; English.
                              Zur Megede J, Barnett SW,
(UYST-) UNIV STELLENBOSCH
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 2460; Conservative
                                                            WPI; 2002-154920/20.
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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|--|--|--|--|--|--|----------------------|--|--|---|--|
| ACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCGTGAAGCCCGGCATG ALL11111111111111111111111111111111111 | AACACCCCGTGTTCGCCATCAAGAAGGACAGCACCCAAGTGGCGCAAGCTGGTCGAC 111111111111111111111111111111111111 | CCCGCCGGCCTGAAGAAGAAGGAGGGTGACGTGCTGGACGTGGGCGACGCCTACTTC [| ACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGGTTTTTTTT | CCCAGCATCTTCCAGAGCAGCAGCAGCTGGGAGCCCTGGAGCCCCTGGAGCCCCCGCAACCCC LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | CAGCACCGCCCAAGATCGAGGAGCTGCGCAAGCACTGCTGCGCTGGGGCTTCACCACC [| | ATCCAGAAGCTGGTGGGAAGCTGAACTGGGCCAGCCAGATCTACCCGGCATCAAGGT CGCCAGCTGTGCAAGCTGCTGCGGGGGCGCCAAGGCCCTGACCGACATCGTGCCCTGAC | GAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCCCTTCACGC | GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACAG | TGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG |
| 661 661 721 721 781 | 841 841 901 | 961 961 1021 1021 | 8 8 • | 1141 1141 1201 1201 | 1255 1261 1315 1321 | 1375 1381 1435 | 1441 1495 1501 | 1555 | 1615 | 1675 |
| 0 | Oy Oy Db | oy Oy | QY Dp | oy Oy | Oy Oy Dp | oy Oy | Db Qy Db | Qy Db | Oy Dp | Qy Dp |

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Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds.
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1735 ATGCGCCACCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAGAAGATCGCC 1794
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                                                       1801 ATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAGGAG
                                                                                                     2101 ACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGGAGGTGAACATCGTG
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                                            1795 ATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAG
                                                                                        1855 ACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTC
                                                                                                                                    GTGAACACCCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGC
                                                                                                                                                1921 GTGAACACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAAGAAGAAGAGCCCATCATCGGC
                                                                                                                                                                                                                                                                         ACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGCAGCGAGGTGAACATCGTG
                                                                                                                                                                                                                                                                                                                     2155 ACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGGGAG
                                                                                                                                                                                                                                                                                     Synthetic construct PR975YMWM SEQ ID NO:32
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17-JAN-2002.

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98.9%; Score 2436.2; DB 24; Length 2457; 99.6%; Pred. No. 3.2e-297; cive 0; Mismatches 3; Indels 6;
                                                               Rensburg
                                                                                                                                                                                                                                       Sequence 2457 BP; 566 A; 837 C; 754 G; 300 T; 0 other;
                                                               Van
                                                               Ś
                                                                                                                                                                                                                        exemplification of the present invention.
                                                              Engelbrecht
                                                                                                                           Claim 1; Fig 10; 233pp; English.
       05-JUL-2001; 2001WO-US21241.
                      05-JUL-2000; 2000US-0610313
                                                             Barnett SW,
                                      (CHIR ) CHIRON CORP. (UYST-) UNIV STELLENBOSCH
                                                                                                                                                                                                                                                                Best Local Similarity 99,6
Matches 2454; Conservative
                                                                             WPI; 2002-154920/20.
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                                                             Megede J,
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                                                                                                                                                                                                                   useful
                                                                                                                                                                                                             New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy
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                                                                                     ACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG
                                                                                                      AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG
                                                                                                                                                            1795 AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG
                                                                                                                                                                                                     GAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCCGAGTGGGAGTTCGTGAAC
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                            TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC
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Gag-reverse transcriptase expression cassette, FS(-)_ProtMod_Rropt_YM.

The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV day of the properties of the particle cassette may be used for the recombinant expression of HIV day of the properties of the particle cassette may be used for the new passion of HIV day of HIV day of the passion of the passio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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83.1%; Score 2046; DB 21; Length 2306;
Best Local Similarity 93.6%; Pred. No. 2.4e-248;
Matches 2159; Conservative 0; Mismatches 135; Indels 12;
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elby M, Walker
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2027.6; DB 24; Lengt
Pred. No. 4e-246;
0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                               New modified human immunodeficiency virus Env, Gag, its encoded protein, useful as vaccines for genetic immunisation for acquired immunodeficiency syndrome immunodeficiency virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 766-769; 794pp; English.
                                                                                                     DEPT HEALTH & HUMAN SERVICES
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3500 TGGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCACAAGGCCATCGGCACCGTGC 3559
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                                                                     TCTGCGAGGAGATGGAGAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACA
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                                                602 TGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCA
                                                                                                                                         CCCTGAACTTCCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG
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                                                                                                                                                       GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCCGCA 4699
                                                                                             TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA 1855
                                                                                                                                                                                         TGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG 1975
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                                               TGCGCACCGCCCACACCAACGACGTGAAGCTGACCGAGGCCGTGCAGAAGATCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
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The present sequence is the coding sequence of a synthetic HIV Gag-reverse transcriptase expression cassette, FS(-)_ProtMod_RTopt(+). The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-enry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGGACCTGCCTGCAGGCCAAGGCCCGCGAGTTCAGCAGCGAGCAGACCCGCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.2%; Score 2025.2; DB 21; Length 2312; Best Local Similarity 93.3%; Pred. No. 9.6e-246; Matches 2156; Conservative 0; Mismatches 138; Indels 18;
                                                                                                                    Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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                                             Hartog
                                                                                                                                                                                                                                                                                                                                                          Sequence 2312 BP; 533 A; 750 C; 732 G; 297 T; 0 other;
                                             Lian Y,
                                           Srivastava I,
C;
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                                           Megede J,
M, Walker
              (CHIR ) CHIRON CORP.
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Greer C,
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          2012 AGACCAAGATCGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGATCGTGAGCC
                                                                                                    1861 AGACCAAGCTGGGCAAGGCCGGCTACGTGACCGACGGGGCCGGCAGAGGTGGTGACGA
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C;
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Selby M, Walker
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01-DEC-1999;
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polypeptide useful for vaccinating against HIV acquired immunodeficiency syndrome (AIDS) -Gag-containing infections and

Claim 7; Fig 74; 391pp; English.

Gag-reverse transcriptase expression cassette, FS(-)_Protbod_Rropt_YMWM. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-pollypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS). present sequence is the coding sequence of a synthetic HIV

Sequence 2300 BP; 528 A; 754 C; 725 G; 293 T; 0 other;

3; Gaps DB 21; Length 2300; 18; 138; Indels Score 2019.2; DB 2. Pred. No. 5.4e-245; 0; Mismatches 82.0%; Best_Local Similarity 93.2 Matches 2150; Conservative Query Match

170 GCGGCAAGGAGGCCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCG 229 δλ

9 Д

ŏ g

180 ACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCG-----ACAACCCCCGCAGCGAGG 121 290 ò g

397 ACAGCCCCACCCGCCGCGAGCTGCAGGTGTGGGGCCGCGAGAACAACAGCCTGAGCGAGG CCGGCGCCGAGGCCACCCTG-----AACTTCCCCCAGATCACCTGTGGCAGC 181 344

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457 GCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCG 398

300 CCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGATCG 458

480 637 GCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCA 578 421 δ g

540 697 ACATGCTGACCCAGCTGGGCTGCACCTTGAACTTCCCCATCAGCCCCATCGAGACCGTGC 481 g ŏ

757 009 CCGTGAAGCTGAAGCCCGGCATGGACGCCCCAAGGTGAAGCAGGTGGCCCTTGACCGAGG 869 541 g ŏ

817 AGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCA AGAAGATCAAGGCCCTGGTGGAGATCTGCACCGAGATGGAGAAGGAGGGCAAGATCAGCA 758 601

pp

Ω

AGATCGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCA 818 561 δλ g

CCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGG 721 δ qq

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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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Modified HIV protein-encoding plasmid DNA #174
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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28-MAR-2001;
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef: Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449 ABK91624 represent modified HIV protein-encoding
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                                                                                                                                                                                                               DB 24; Length 9788;
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified human immunodeficiency virus Env, Gag, Pol of Nefits encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human
                                                                                                                                                                                                                                                                                                     GCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTA 2387
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
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                                                                                                                                                                                              Query Match 81.4%; Score 2005.2; DB 24; Length 9169; Best Local Similarity 91.4%; Pred. No. 2.5e-243; Matches 2187; Conservative 0; Mismatches 183; Indels 22;
                                                                                                                                                                  Sequence 9169 BP; 2227 A; 2668 C; 2505 G; 1769 T; 0 other;
                                                                                                                                    plasmid DNA sequences of the invention.
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CIL.
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                                                                                                                                 CCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCGAGGTGAACATCGTGA 2155
                                                                                                                                                                                New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
CCGAGACCTTCTACGTGGACGCGCCGCCAACGAGCCAAGATCGGCAAGGCCGGCT
                                                            CCGAGACCTTCTACGTGGACGCCCCCCAACCGCGAGACCAAGCTGGGCAAGGCCGGCT
                                                                                   CCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCGACCCGACAAGAGCGGAGC
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The invention relates to a nucleic acid molecule encoding a modified HIV

Page 753-756; 794pp; English.

Disclosure;

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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for penetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired in munodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef: Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ARK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
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                                                                                                                                                                                                                               81.3%; Score 2001.8; DB 24; Length 9194; 91.3%; Pred. No. 6.8e-243; ive 0; Mismatches 187; Indels 22; (
                                                                                                                                                                                              Sequence 9194 BP; 2232 A; 2672 C; 2523 G; 1767 T; 0 other;
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Matches 2186; Conservative
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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(CHAD/) CHADRABARTI B K.
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The invention relates to a nucleic acid molecule encoding a modified HIV

English,

Disclosure; Page 750-753; 794pp;

(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquires in particular immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Gag, Pol or Nef. Furthermoze, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.

Sequence 9194 BP; 2232 A; 2671 C; 2524 G; 1767 T; 0 other;

5, 3146 3445 TGGCCGAGGCCATGAGCCAGGTGACCAACAGCGCCACCATCATGATGCAGCGCGCGAACT 3026 TCCGCAACCAGCGCAAGATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCCACACCGCCC 3086 538 GCAACTGCCGCGCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGA 190 718 778 22; Gaps 3626 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCGGGCA TCAAGGGCCCCAAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC TGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG TGCAGGTGCGCGG-----CGACAACCCCCGCAGGCAGGCCGGCGGCGAGCGCCAGGGCA TTCAGGTTTGGGGAAGAGACAACACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAA GCAAGGCCCGCGAGTTCCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGC AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGGCATCGGCGGCTTCATCA -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGGCATCAAGG AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGG TGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG CCATCTGCGAGGAGATGGAGGAGGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT 9194; 24; Length Pred. No. 1.1e-242; ; Mismatches 188; Indels Score 2000.2; DB ; Query Match
Best Local Similarity 91.2%;
Matches 2185; Conservative 0 Query Match 3027 3206 14 71 3087 311 365 3446 3506 2967 131 419 479 3566 191 3147 251 599 629 85555555555%8 ŏ g Ω P Qγ g δ g Ω qq ò qq οy g qq QQ Dp g Db ò δ QΫ́ δ ò δy

1018 1252 1312 1672 4645 4705 1913 TCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGGAGGAGGCCCATCATCG 1972 ACCCGCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCACCCAGCATCA 1079 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA ACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG ACTICCGCGAGCIGAACAAGCGCACCCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCC GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGGCAACC CCGAGATCGTGATCTACCA-----GGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGCTACGAGCTGCACC CCGAGGAGGCCGAGCTGGCCGCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1733 AGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA 1373 CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG ACATCCAGAAGCTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGG GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 4586 GCGTGTACTACGACCCCAGCAAGAACTGCTGATCGCCGAGATCCAGAGCAGGGCCAGGCC CCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC 4706 GCATGAAGGCCCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG AGACCTGGGAGACCTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT 1019 3806 3986 4046 1139 1199 4166 1253 1313 4286 4346 1433 1493 4526 1613 1673 4646 839 4106 4226 4406 4466 1553 1793 1853 qq Qγ OD Db ò Pp δ g q ò QY Q g Qγ QQ δ q qq QQ q δ ò QΥ ŏ g δy g QY g ŏ g g ò ŏ δ

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The invention relates to a nucleic acid molecule encoding a modified HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA Its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human
                                                                                                                                                                      AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG
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 TCGTGAACACCCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG
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                                 GCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCG
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                encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for appropriate or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
(human immunodeficiency virus) protein. The nucleic acid molecule and its
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                                                                                                                                                                              plasmid DNA sequences of the invention.
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Best Local Similarity 91.2%;
Matches 2185; Conservative
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Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS;
acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for appearation or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91674 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
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Sequence 9785 BP; 2360 A; 2843 C; 2731 G; 1851 T; 0 other;

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0; Mismatches 182; Indels
81.1%; Score 1996.8; DB 24;
91.3%; Pred. No. 2.8e-242;
             Best Local Similarity 91.3
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2276 CCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCC 2335
<u> ACGTGACCGACCGCCGCCAGAAGGTGGTGCCCCTGACCGACACCACAACCAGAAGA</u>
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK9149-ABK91624 represent modified HIV protein-encoding
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                                                                                                                                                                                                                                             DB 24; Length 9167;
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         ACCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT
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                                    ACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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4878 TCGTGAACACCCCCCCCCCCCTGGTGAAGCTGGTGCTACCAGCTGGAGAAGCACCCCATCATCG
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(human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV BrV, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV BrV, Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91634 represent modified HIV protein-encoding plasmid DNA sequences of the invention.

Sequence 9170 BP; 2225 A; 2669 C; 2519 G; 1757 T; 0 other;

ů, GGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGAGC 3260 TCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCC 130 GCAACTGCCGCCCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCCAAGGAGGGCCACCAGA 190 310 418 TGAAGGACTGCACGAGGCCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG TGCAGGTGCGCGG-----CGACAACCCCCGCAGGGCCGGCGCCGAGGCCCAGGGCA AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGGATCGGCGGCATCGGCGGCTTCATCA GCAAGGCCCGCGAGTTCCCCAAGCGAGCAGCGCGCCAAACAGCCCCAACAGCCGCGAGC -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGG TGGGCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGG 24; Length 9170; 0; Mismatches 186; Indels 80.9%; Score 1993.4; DB 24 91.1%; Pred. No. 7.6e-242; Best Local Similarity 91.1 Matches 2182; Conservative Match 2967 3087 3321 3381 14 7.1 3027 3147 251 3201 3261 131 191 311 365 419 479 Query Οy Q ŏ ò Q qq Q Qγ g Óγ qq Óλ Q ò Вb òγ g

AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGACCATCGGCAACGA TGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT TGCTGGTGGGCCCCACCCCGTGAACATCGGCCGCAACCTGCTGACCCAGATCGGCT GCACCCTGAACTTCCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA CCATCTGCGAGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT TGGACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 3501 3561 3621 599 629 719 Db Ω q Ω Db QΥ g ŏ Q δ

1492 1018 1312 1432 4400 1612 1792 GCATGAAGGCCCCCCACCCAACGACGTGAAGCAGCTGACGAGGCCGTGCAGAAGATCG 4760 1912 TCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG 1972 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCCAGGGCTGGAAGGGCA TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA ACATCCAGAAGCTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGG ACAACACCCCCGTGTTCGCCATCAAGAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG ACCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGGCGACGCCTACT 4041 ACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC CCGAGATCGTGATCTACCA-----GGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGCTTCACCA CCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG CCGAGGAGGCCGAGCTGGACTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG CCGAGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGCCCGTGCACG AGTIGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1733 AGATGCGCACCGCCCACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGGAGGTGCAGCTGGGCATCCCCC TGCGCCAGCTGTGCAAGCTGCTGCGGCGCACCAAGGCCCTGACCGAGGTGGTGCCCCTGA GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT 1019 3801 959 3921 1079 4101 1199 4161 4221 1313 4281 1373 1433 4401 4461 4521 1613 4581 1673 4641 1793 4761 1853 4821 1913 839 899 1139 1253 1493 1553 4701 Q ò δ qq óλ Dp Óγ pp δ QQ Ω QQ δý g g g Dp Dp ò ά δ Ω δλ g δ g QΥ q ŏ 셤 g öλ d ŏ δ

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BM372120 EBro03_SQ BM368580 EBem08_SQ AJ471121 AJ471121

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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 2598)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Anthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Opergo Probes
Unpublished (2002)

2 (bases 1 to 2598)
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. 2598
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/db_xref="MaizeDB:638378"
/db_xref="taxon:4577"
/clone="PCO142084"
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BM321023
BM321393
BMS67428
BE601575
BM372120
BM36580
AJ471121
BQ464692
BM377112
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BQ765498
AL508778
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Zea mays
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Compugen Ltd.
                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                   16154066 segs, 8097743376 residues
     GenCore version
Copyright (c) 1993 - 2003
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BO464622 HF02P20r BM377112 EBem05_SO BM377112 EBem05_SO BM372871 EBmad4_SO BM372871 EBmad4_SO BM372871 EBmad4_SO BM372875 EBr008_SO BM37022 EBr008_SO BM37022 EBr008_SO BM37022 EBr008_SO BM37022 EBr008_SO BM37022 EBr008_SO BM37023 EBr008_SO BM37023 EBr008_SO BM37023 EBr008_SO BM37023 ALSOBS13 BM584191 170006873 BM584191 170006873 BM584191 170006873 BM584191 170006873 BM584191 170006873 BM584191 170006873 BM584192 947029E04 BM384122 947029E04 BM384122 947029E04 BM384122 947029E04 BM384122 947029E04 BM384114 BM384 BM38411 BM38451

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                                                      /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" 406 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1136 GCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCA 1195
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         716 GCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 AGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCA
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                                                                                                                                                                                                                                                                                                                                                      3.5%; Score 86.8; DB 11;
Similarity 42.1%; Pred. No. 6.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 1102;
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                                                                                                                                                                                   1005 CGGGGTCCATCGAGGCCGCGCCCATCATGGAGCACATCCTGGATGGCAGCTCCTTCATGA 1064
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888 IGTACGACGCCAACGTCCTGGCCGTCCTGTCGGAGGTCCT---GTCCGCCGTCTTCTGCG
                                                                                                                                          1256 AGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGCGCTGGGGGCTTCACCACCC
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                                                                                                                                                                                                                                                                                                                                                                       1125 CGCTCCGCACGTCGCCGCAGTGGCTGGGCCCCCAGATCGAGGTC---ATCCGCGCCCCA
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                                              1196 ACCCCGAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCC
                                                                                                                                                                                                                                                                             1065 AGCAGGCCAAGAAGTTGAACGAGCTGGACCCGCTGCTGAAGCCCCAAGCAGGACAGGTACG
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/clone_lib="Mastigamoeba balamuthi lambda 2AP II Library"
/note="syn: Phreatamoeba balamuthi"
                                                         rockefeller.0.1211 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to adenosylhomocysteinase (EC 3.3.1.1), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
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                                                                                                                                                                                                                                                                                          Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.
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1 (bases 1 to 951)
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46.0%; Pred. No. 0.0001;
tive 0; Mismatches 376; Indels 3
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/organism="Mastigamoeba balamuthi"
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                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmuller@rockvax.rockefeller.edu
Insert Length: 951 Std Error: 0.00
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Matches 323; Conservative
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BM320864 1132 bp mRNA linear EST 03-JAN-2002 rockefeller.0.46 Mastigamoeba balamuthi lambda ZAP II Library
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/db_xref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi"
/note="syn: Phreatamoeba balamuthi"
/ 413 c 324 g 171 t 4 others
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1 (bases 1 to 1132)
1 Bapteste; E. Brinkmann, H. Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostellum, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                   2208 GAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAG 2267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 CGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCCAAGGAGGGCCACCACAATGAAGGAC 198
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                                                                                                                                                                                                                                                                                                                       816 CGGCCAGGGCTGCCGCGTCATCGTGACGGAGATCGACCCCATCTGCGCGCTGCAGGCGTC 875
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639 GTTCCCGGCCGTCAACGTCAACGAC---TCTNTCACCAAGAGCAAGTTCGACAACATCTA 695
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                                                                                                      696 CGGCTGCCGCCACTCGCTCATCGACGGCATCAAGCGCGGCACGACGTGATGCTCGGCGG
                                                                                                                                                           2268 CTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGGAGTGGACAAGCTGGTGAGCAA
                                                                                                                                                                                                              756 CAAGGTCGCCGTCGTCGCGGGCTACGGCGACGTGGGCAAGGGCTGCGCCGAGTCGCTGCG
                                                                                                                                                                                                                                                                    2328 GGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTA
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1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mastigamoeba balamuthi.
Mastigamoeba balamuthi
Mastigamoeba balamuthi
Eukaryota; Pelobionida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1165)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
                     312
                                                                                                                                                                                                                                                                                                                                                        GCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAG 498
                                                                                                                                                                                                                           TTCAAGGCCCTGCTCGACGTCGGCCTGGTCCGCACCTCGACTGGCGCCCGCGTGTTCGCC 492
                                                                                                                                                                                                                                                                                                                                                                                                       679 AGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAG 738
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                                                                                                                                           253 GAGCTCACCGGCTTCGGCGTCAAGCTCGGCCTGACCAACTACGCCGCCGCCTACGCGACT
                                                  CAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAG
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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                                                                                                                                                                                                                                                                                                          90 CATCAAGTGCTTCAACTGCGGCAAGGAGGCCCACATCGCCCGCAACTGCCGCGCCCCCCG
                                                                                                                                                                                                                                                                                                                                                             46 CGTCAAGAACAAGGCGTACTTCAAGCGCTTCCAGACCCAGTTCCGTCGCCGCGCGAGGG
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                                                                             balamuthi lambda ZAP
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                                                                                                                               4 others
                                                                                                                                                                                                       Score 79.6; DB 13; Length
Pred. No. 0.001;
0; Mismatches 506; Indels
                                               /db_xref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi 1
/note="syn: Phreatamoeba balamuthi"
426 336 9 178 t 4 o
/organism="Mastigamoeba balamuthi"
/strain="ATCC 30984"
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Best Local Similarity 45.1'
Matches 428; Conservative
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/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
                                                                                                     BM321430 867 bp mRNA linear EST 03-JAN-200 rockefeller.0.1153 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to ribosomal protein S4, mRNA
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 10 867)
Bapteste, E., Brinkmann, H., Lee, J. A., Moore, D. V., Sensen, C. W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
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930 CGGTGCCCTGTACACCGCCATCTCCCCGCTGCGGCGTTGCGCTGCTTGCGG 979
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/strain="ATCC 30984"
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmullerfockvax.rockefeller.edu
Insert Length: 867 Std Error: 0.00
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BM321022 1550 bp mRNA linear EST 03-JAN-2002 rockefeller.0.1192 Mastigamoeba balamuthi lambda 2AP II Library Mastigamoeba balamuthi cDNA similar to adenosylhomocysteinase (EC
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/note="syn: Phreatamoeba balamuthi"
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Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
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Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
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GAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTC
                                                   551 TTCGAGATCGGCAACCTCGTCATGATCACTGGCGGACGCAACCTTGGCCGCGTCGGCGTC
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1550)
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45.6%; Pred. No. 0.0032;
tive 0; Mismatches 364; Indels 3;
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1550 Std Error: 0.00
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Laboratory of Biochemical Parasitology
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/strain="ATCC 3084"
/db_xref="taxon:108607"
/db_xref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
294 c 260 g 126 t 7 others
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                                                                                    2295 CGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGA 2354
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                1935 GAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGA 1994
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Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
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                                       185 CCACAAGGGGTTCGCGCCGAGGACAACCCCAAGCTGCTGGAGGACGACGAGGGCCTCGA
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The Rockefeller University
1230 York Avenue, New York, NY 10021, I
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BM321023
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Mastigamoeba balamuthi
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BM321393 853 bp mRNA linear EST 03-JAN-2002 rockefeller.0.1222 Mastigamoeba balamuthi lambda 2AP II Library Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA
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The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                            1848 GAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTG 1907
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                                                                                                                                                                                                                                                                                                            280 CATCGCGCAGGCCGGAGTCTCGGCTTTCGCCTGGAAGGGCGAGAACCTCCAGGAGTACTG 339
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                                                                                                                                                                                                                                                                         1788 GATCGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640 GTTCCCGGCCGTCAACGTCAACGACTCTGTCACCAAGAGCAAGTTTGACAACATCTACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2205 CGAGAGCGAGCTGGTGAACCAGATCATCGAGCTGATCAAGAAGGAGAAGGTGTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 CGAGGAGACGACTGGCGTGATGAGGCTGTACCAGCTGCACCGCGACGGCAAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2148 CATCGTGACCGACAGCCAGTACGCCCTGGGCATC---ATCCAGGCCCAGCCCGACAAGAG
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1 (bases 1 to 853)
   Length 862
                                                                   0; Mismatches 327; Indels
Score 75; DB 13;
Pred. No. 0.0057;
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3.0%;
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Query Match
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         ORGANISM
                                                                                                                                  TITLE
JOURNAL
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                                                                                                                                         /strain="ArCC 30984"
/db_xref="taxon:1088607"
/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
                                                                                                                                                                                                                                                                                                                                      388 CTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGCCGGCCAGATCAAGGAGGCCCTGCTG 447
                                                                                                                                                                                                                                                                                                                                                                                                            448 GACACCGGCGCCGACGACGACGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCC 507
                                                                                                                                                                                                                                                                                                                                                                         125 CIGGCCCGCCGTGTGCTGAAGAAGCTCAACCTCGAAGTACGAGGGTGTCAAGAAG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 CTGCTCGACGTCGGCCTGGTCCGCACCTCGACCGGCGCCCCGCGTGTTCGCCGCCCCCAAG 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868 AAGGACAGCACCAAGIGGCGCAAGCIGGIGGACTICCGCGAGCIGAACAAGCGCACCCAG 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        928 GACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGC 987
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                                                                                                                                                                                                                                                                    Score 73.2; DB 13; Length 853;
Pred. No. 0.011;
0; Mismatches 329; Indels 9
                                                                                                                                                                                                                      2 others
                                                                                                                           /organism="Mastigamoeba balamuthi"
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                1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 853 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 CCCGGTGCCCTGTACACNGCCATCTCCCGCTGCGGCG 752
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The Rockefeller University
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BMS87428 566 bp mRNA linear EST 25-FEB-2002 17000687321202 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449696110 5', mRNA sequence.

RESULT 9 BM587428/c

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DEFINITION

ACCESSION

KEYWORDS

African malaria mosquito. BM587428.1 GI:18883289

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                                                                                              Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab J.R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project Onpublished (2002) Contact: Holt R.A. Celera Genomics 45 w. Gude Dr., Rockville, MD 20850, USA Fer: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitces (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. CDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3. Clones available through the Malaria Research and Reference Research Resource Center (www.malaria.mr4.org)" 202 c 165 g 139 t.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 GAAGATCAAGTGGCTGGACGAGAACCAGGACACCGAGGCGGAAGAGTACAAGAAGCAGAA 123
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                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="RSP-ST (Reduced susc. to Permethrin - std.
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="19600449696110"
/clone=1"h="A.gam.ad.cDNA.blood1"
/dev.stage="Adult"
/lab_host="PH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gambiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               Email: HoltRA@celera.com
Plate: NU01004AAX row: C
Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome)"
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Anopheles gambiae
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And Just Street 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 640)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu,
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0098K08f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/Dgn/31/cover.html)" 230 c 177 g 97 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
On May 21, 2000 this sequence version replaced gi:13190104.
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/db_xref="mexcon:4513"
/clone="HvSMBh0098K08f"
/clone=lib="Hordeum vulgare 5-45 DAP spike EST library
HvCnNACQP 5- 5- 45 DAP)"
/tlssue_type="5-45 DAP Spike"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
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/organism="Hordeum vulgare"
/cultivar="Morex"
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High quality sequence stop: 534.
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                                                                                                                                              BE601575.3 GI:16322423
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Fax: 864 656 4293
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1089 CCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCAGCAT 1148

410 CCGCAACTICCTCGGCGAGAAGAAGGTGAGGAAGGTGGACATGCTCGACGGGGTCACCAT

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969 CCTGAAGAAGAAGAAGGGTGACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCC 1028

230 GCTCAAGGTGGACGCCTGGTTCGGCACCCGCCGCACCATGGCCGCCATCCGCACCGCCAT 289

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1149 CTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCCCCAACCCCGAGATCGT 1208

470 CTTGCGGTCCGAGAAGGTCAAGGATGAGATCGTCCTCGACGCCAACGACATCGAGCTCGT 529

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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 500)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Hansay, L., Machray, G., Marshall, D. F. M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Jan 10, 2002 this sequence version replaced gi:18115510.
Contact: Waugh R. Marshall DF
Genome Dynamics/Computational Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: psport1; Site_1: Sal 1; Site_2: Not 1; Non-normalised library, directionally cloned into psporT1. Non-normalised from roots of 3 week old waterlogged barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                    BBM372120 500 bp mRNA linear EST 23-JUL-2002 EBRO03_SQ004_B09_R root, 3 week, waterlogged, cv Optic, EBro03 Hordeum vulgare cDNA clone EBro03_SQ004_B09_5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All sequence has a Phred quality score of 20 or over Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
TTE1: 00 44 1382 562731
Fax: 00 44 1382 562426
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/db_xref="taxon:4513"
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/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@scri.sari.ac.uk
                                                                                                                                                                  BM372120.2 GI:21948499
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Query Match 2.9%; Score 72.2; DB 10; Length 640; Best Local Similarity 47.7%; Pred. No. 0.016; Matches 209; Conservative 0; Mismatches 229; Indels 0;

0; Gaps

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ENGAURA VILIGIPLE Streptophyta; Embryophyta; Tracheophyta; Spermatorphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordcum, Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordcum, Magnoliophyta; Liliopsida; Poales; Pooideae; Triticeae; Hordcum, Magnoliophyta; Liliopsida; Caldwell,D. McCallum,N., Mudie,S., Cardle,L., Ransay,L., Machray,G., Marshall,D.F.M. and Waugh,R.

Development of Barley Transcriptome Resources
AL Upublished (2001)
On Jan 10, 2002 this sequence version replaced gi:18111970.
Contact: Waugh R, Marshall DF Scottish Crop Research Institute
Invergowrie, Dundee, Dis 562731
Fax: 00 44 1382 562731
Fax: 00 44 1382 562731
Fax: 00 44 1382 562456
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
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EBem08_SQ004_A06_R embryo, 40 DPA, no treatment, cv Optic, EBem08
Hordeum vulgare cDNA clone EBem08_SQ004_A06 5', mRNA sequence.
BM368580
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                                                                                                                               Gaps
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                                                                                     Length 500;
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/cultivar="Optic"

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//note="105"/ University of the property of days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
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                                    /clone_lib="embryo, 40 DPA, no treatment, cv Optic, EBen08"
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Barley EST's
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47.7%; Pred. No. 0.02;
tive 0; Mismatches 229;
                       /clone="EBem08_SQ004_A06"
/db_xref="taxon:4513"
                                                                                                /tissue_type="embryo"
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Contact: Schulman AH
Institute of Biotechnology
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1. Triticeae; Hordeum.

1. (bases 1 to 566)

Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.

Barley ESTs from developing seeds
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGTTCGCCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGA 908
University of Helsinki
P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
                                                                                                                                                                                                                                                                                                                                     0; Gaps
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HF02P20r HF Hordeum vulgare cDNA clone HF02P20 5-PRIME, mRNA
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                           Query Match 2.9%; Score 71.6; DB 9; Length 540; Best Local Similarity 47.7%; Pred. No. 0.02; Matches 209; Conservative 0; Mismatches 229; Indels
                                                                                                   /organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone="$0000001911A10F1"
/clone_lib="$00008"
/tissue_type="Callus"
/note="Callus K19"
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                                                              Location/Qualifiers
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/_note="vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); developing caryopsis 16-25 DAF(days after flowing) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.Average insert size is 940 bp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 23-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="developing caryopsis, 16-25 DAF (days after
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                                                    6 Std Error: 0.00 column: 20
                                                                                                                                                                                                           /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="caryopsis"
Fax: 039482-5595
Email: stein@ipk.gatersleben.de
Insert Length: 566 Std Error:
Plate: 2 row: P column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="XL10-Gold"
                                                                                                                                                                                                                                                         /db_xref="taxon:4513"
/clone="HF02P20"
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                    /cultivar="Barke"
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BM377112.2 GI:21934595
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KEYWORDS
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/note="Vector: pSPORT1; Site_1: Sal 1; Site_2: Not 1; Non-normalised library, directionally cloned into pSPORT1. Derived from embryos dissected from developing grains (14 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBRRC/SERRAD funded cereal IGF (Investigating Gene Function) project."
                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Optic" // Cultivar="Optic" // Cultivar="Optic" // Ob xref="taxon:4513" // Clone="EBem05_80004_C16" // Clone="EBem05_80004_C16" // EBem05 // Clone_Lib="embryo, 14 DPA, no treatment, cv Optic, EBem05"
                                                                                                            DB 13; Length 578;
                                                                                                                                                                                                                                                                                                                                                                                       Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
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Scottish Crop Research Institute
Invergentie, Dundee, DD2 5DA, Scotland, UK
TTE1: 00 44 1382 562731
Fax: 00 44 1382 562426
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47.7%; Pred. No. 0.02;
tive 0; Mismatches 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 reverse.
Location/Qualifiers
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/lab_host="DH10B"
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Matches 209; Conservative
  Hordeum vulgare.
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTus_comB.seq:*
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| No. | Score | Match | Length | DB | ID | Description |
| 1 | 1106.8 | 44.9 | 2601 | 4 | 117 | Sequence 7, Appli |
| 7 | 1106.8 | | 2601 | 4 | US-09-117-217-9 | 9 |
| 3 | 1106.8 | | 2601 | 4 | 117 | 11, |
| 4 | 1106.8 | 44.9 | 2601 | 4 | US-09-117-217-13 | 13, |
| ហ | 1100.4 | | 7399 | ~1 | -08 | 6 |
| 9 | 1100.4 | 44.7 | 9709 | 7 | US-08-188-583-5 | 'n |
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| 13 | 1100.4 | • | 15581 | 4 | US-09-503-222-35 | 35, |
| 14 | 1090.8 | 44.3 | 9737 | 7 | US-08-944-449-7 | 7 |
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| 16 | 1055.6 | 42.9 | 9746 | П | US-08-022-835-3 | 3, |
| 17 | 1055.6 | 42.9 | 9746 | Н | -08-388 | 3, |
| 18 | 1055.6 | 42.9 | 9746 | ~ | -08-647-714 | ς, |
| 19 | 1054.4 | 42.8 | 8932 | 4 | -09 | ı, |
| 20 | 1054.4 | 42.8 | 8933 | m | US-08-463-210-4 | 4, |
| 21 | 1054.4 | 42.8 | 8933 | 4 | US-09-620-958A-3 | 'n |
| 22 | 1054.4 | 42.8 | 8933 | 4 | -60- | 4 |
| 23 | 1054.4 | 42.8 | 8933 | 4 | -620-9 | 6 |
| 24 | 1042 | 42.3 | 9739 | П | -08 | ı, |
| 25 | 1042 | 42.3 | 9739 | Н | US-08-388-809-1 | Ļ |
| 26 | 1042 | 42.3 | 9739 | 7 | US-08-647-714-1 | ı, |
| 27 | 1036.8 | 42.1 | 5362 | m | US-08-463-210-5 | 5, |
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| Sequence 19, Appl Sequence 21, Appl Sequence 800, App Sequence 20, Appl Sequence 16, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 5, Appl Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli | OTHERAPY OF PATIENTS WHO ARE PHENOTYPIC DRUG SENSITIVITY | Length 2601; Indels 22; Gaps 5; ATGCAGCGCAGCAACT 70 |
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| 2 US-07-743-357-19 2 US-07-743-357-21 3 US-08-388-353-800 3 US-08-488-5518-800 2 US-07-743-357-20 2 US-07-743-357-16 2 US-07-743-357-16 2 US-08-976-546A-1 4 US-09-912-55-1 1 US-08-470-202-56 1 US-08-470-202-56 2 US-08-470-202-56 3 US-08-468-059-56 4 US-09-109-916-56 5 PCT-US-3-06748-1 6 US-09-158-695-18 6 US-09-256-490-14 6 US-09-256-490-14 | ALIGNMENTS 117217 -Pierre F MANAGING THE CHEM HIV STRAINS US/09/117,217 -24 | tch al Similarity 68.2%; Pred. No. 1.4e-173; 1618; Conservative 0; Mismatches 732; Indels 22; G TGGCCGAGGCCATGAGCCACCAGCGCCAACATCCTGATGCAGCGCACCACT |
| 41.6 41.6 41.4 41.4 41.4 41.4 41.4 41.4 | ·- 2 | ch 1 Similarity 68 618; Conservative 6GCCGAGGCCATGAGCCA 1 |
| 28 1025 30 1025 30 1019.2 31 1019.2 32 43.6 843.6 843.6 843.6 831 831 831 831 831 831 831 831 | SULT 1 Sequence 7, Applicat Sequence 7, Applicat Sequent No. 6221578 GENERAL INFORMATION: APPLICANT: HERTOGS, APPLICANT: HERTOGS, APPLICANT: PAUWELS, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 137 CURRENT FILING DATE CURRENT PELLING DATE CURRENT FILING DATE CURRENT FOR SEQ ID NO SOFTWARE: PACHOLIN SEQ ID NO SOFTWARE: PACHOLIN TYPE: DNA TYPE: DNA TYPE: DNA CENCYMIN: 2601 TYPE: DNA CENCYMIN: 2601 TYPE: DNA CENCYMIN: 2601 TYPE: DNA CORAINO: (1)(49 COCATION: (1)(49 COCATION: (1)(49 | Query Match Best Local Sin Matches 1618; 14 TGGCCC 11 TGGCCC 71 TCAAGG 71 TCAAGG 137 TAGGAP 111 TGAAGG 191 TGAAGG 191 TGAAGG 251 TGAAGG 111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
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| Qy Dp | 311 | TGCAGGTGCGCGGCGACAACCCCCGCGGGCGGGGCG | |
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| Oy Db | 365 | 41 | |
| Qy Db | 419 | 47 55 | |
| Qy Db | 479 | AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCA 538 | |
| Qy | 539 | AGGIGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG 598 | |
| Oy Db | 599 | TGCTGATCGGCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT 658 | |
| Qy Db | 659 | GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGACCTGAAGCTGAAGCCCGGCA 718 | |
| Qy Dp | 719 | TGGACGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 778 | |
| Qy Db | 9779 | CCATCTGCGAGGAGAAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT 838 | |
| Oy Db | 839 | ACAACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG 898 | |
| Qy Dp | 999 | ACTICCGCGAGCTGAACAAGCGCACCCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCC 958 | |
| Qy Db | 959 | ACCCGCCGCCTGAAGAAGAAGAAGAGCGTGACCGTGGTGGACGTGGGCGACGCCTACT 1018 | |
| Qy | 1019 | TCAGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 1078 | |
| Qy Db | 1079 | ACAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGC 1138 | |
| Qy Dp | 1139 | GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCCGCAACC 1198 | |
| Qy Db | 1199 | CCGAGATCGTGATCTACCAGGCCCCCTGTACGTGGCAGCGACCTGGAGATCG 1252 | |
| Qy | 1253 1336 | GCCAGCACCGCGCCAAGATCGAGGAGTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA 1312 | |
| oy Ob | 1313 | CCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC 1372 | |
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                                                                                       1576 TAAGGCAATTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAA
                                                                                                                 CCGAGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG
                                                                                                                                     1636 CAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGTTCTAAAAGAACCAGTACATG
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                               1853 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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RESULT 2
US-09-117-217-9
Sequence 9, Application US/09117217
Patent No. 6221578
GENERAL INFORMATION:

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                                               TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REPERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 TGGCTGAAGCAATGAGCCAAGTAACAATTCAGCTACCATAATGATGCAGAGAGGCAATT 136
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        Query Match
        44.9%;
        Score 1106.8;
        DB 4;
        Length 2601;

        Best Local Similarity
        68.2%;
        Pred. No. 1.4e-173;

        Matches 1618;
        Conservative
        0;
        Mismatches 732;
        Indels 22;

APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: HERTOGS, Kurt
                                                                                                                                                                                                                                                                                          ; LOCATION: (334)..(489)
; OTHER INFORMATION: gag P6 (52 AA)
US-09-117-217-9
                                  APPLICANT: PAUWELS, Rudi
                                                                                                                                                                                                                                             ORGANISM: HIV-HXB2
                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                          ENGTH: 2601
                                                                                                                                                                                                                              TYPE: DNA
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                                                          779 CCATCIGCGAGGAGAIGGAGAAGGAGGGCAAGAICACCAAGAICGGCCCCGAGAACCCCT
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                   959 ACCCCGCCGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGCGACGCCTACT
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APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: HERTOGS, Kurt
APPLICANT: PAUMELS, Rudt
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REPERENCE: 1377-1229
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VEY: 2.0
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1876 CCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAACTGCCCATACAAAGG 1935
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                                                1853 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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71 TCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130
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                                                                                                      131 GCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGA
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TYPE: DNA ORGANISM: HIV-HXB2
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               1576 TAAGGCAATTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAA 1635
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1139 GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCCAACC 1198
                                                         1199 CCGAGATCGTGATCTACCA-----GGCCCCCTGTACGTGGGCAGCGACCTGGAGATCG 1252
                                                                                                                1253 GCCAGCACCGCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCTGCGGCCTTCACCA 1312
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APPLICANT: PAUMELS, RUdi
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: HIV POSITITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REPERBENCE: 1377-1259
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 13
2296 AGTTAGTCAATCAAATAATAGAGCAGTTAATAAAAAGGAAAAGGTCTATCTGGCATGGG 2355
                                                                                                                                      2356 TACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAA 2415
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Pred. No. 1.4e-173;
0; Mismatches 732; Indels
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; OTHER INFORMATION: Reverse Transcriptase US-09-117-217-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de BETHUNE, Marie-Pierre APPLICANT: HERTOGS, Kurt
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09117217
Patent No. 6221578
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Best Local Similarity 68.2%;
Matches 1618; Conservative
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| ž q | 539 | AGGTGCGCCAGTACGACAGATCCTGATCGAGATCTGCGGCAAGGAGGCCATCGGCACCG 5 1 1 1 1 1 1 1 1 1 | 98 75 |
| 2 <u>7</u> | 599 | TGCTGATCGGCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT 6 | 3 3 35 |
| 2 <u>y</u> | 659 736 | GCACCCTGAACTTCCCCATCAGCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA 7 | 18 95 |
| 27 QC | 719 | TGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAAGATCAAGGCCCTGACCG 7 | 78 55 |
| Sy Op | 779 856 | 0 4 | 38 15 |
| 27 Ob | 839 916 | ACAACACCCCCGGGTTCGCCATCAAGAAGAAGACACACAACATGGCGCAAGCTGGTGG 89) | 98 75 |
| ZY QC | 999 | ACTICCGCGAGCIGAACAAGCGCACCCAGACTICIGGGAGGTGCAGCTGGGCAICCCCC 9: | 58 035 |
| 27 29 | 959 1036 | ACCCGCCGGCCTGAAGAAGAAGAGGTGGCCTGCTGCTGGACGTGGGCGACGCCTACT 1(| 018 095 |
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| λ Q | 1079 | ACAACGAGACCCCCGGCATCCGCTACCAGTACCAACGTGCTGCCCCAGGCTGGAAGGCA 11 | 138 |
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| Zi qi | 1253 1336 | GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA 13 | 312 395 |
| <u>⊁</u> 4 | 1313 1396 | 7 7 | 372 455 |
| ₽ 4 | 1373 | CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACG 14 | 132 |
| <u>⊁</u> 4 | 1433 1516 | ACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCA | 92 |
| <u>⊁</u> a | 1493 | TGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCACGACATGGTGCCCCTGA 15 | 1552 |

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                                                                                                                                  1673 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA
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APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANJERJEA, AKHIL
TITLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2416 TCAGGAAAGTACTATTTTAGATGGAATAGAT 2447
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NEW YORK
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COUNTRY: U.S.A.
ZIP: 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                           44.7%; Score 1100.4; DB 2; Length 7399; 68.0%; Pred. No. 1.7e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 736; Indels
                                                                                                                                                                                                                                            2026-4091US2
                                                                                        APPLICATION NUMBER: US/08/418,848A
FILING DATE: 07-APR-1995
                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                  07/936,849
                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                           NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 202
                                                                                                                                                                                                                                                                                                       TELEX: 421792
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/93
FILING DATE: 28-AUG-1992
                                                                                                                                                                              CLASSIFICATION: 526
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7399 base pairs
                                                         SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 1614; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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EDNESS: single
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                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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599 IGCTGATCGGCCCCACCCCGTGAACATCATCGCCCGCAACATGCTGACCAGCTGGGCT
                                                   2437 TATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTGGCT
                                                                                                                                                                                                                             719 TGGACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG
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                                                                                                             659 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
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3517 AATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAATATGCAA 3576
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                                                                                                                                  1793 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1852
                                                                                                                                                                         3637 CCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAATTACCCATACAAAGG 3696
                                                                                                                                                                                                                1853 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCCGAGTGGGAGT 1912
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GENERAL INFORMATION:
APPLICANT: Destosiers, Ronald C.
TITLE OF INVENTION: PRIMATE LENTIVING VACCINES
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPTRY: U.S.A.
ZIP: 03.10-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPRATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2333 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CITY: Boston
STATE: Marr
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US-08-188-583-5
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                                                                                                                                                                                                                                                                                                                                                                  Length 9709;
                                                                                                                                                                                                                                                                                                                                                               44.7%; Score 1100.4; DB 2; Length 68.0%; Pred. No. 1.7e-172; tive 0; Mismatches 736; Indels
                                                                                                                        Reg. No. 5851813 29,066
IR: 00246/079002
                                                APPLICATION NUMBER: 07/551,945
FILING DATE: July 12, 1990
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 07/727,494 FILING DATE: July 9, 1991 PRIOR APPLICATION DATA:
                                                                                                   NAME: Freeman, John W.
REGISTRATION NUMBER: Reg. NO.
REFERENCE/DOCKET NUMBER: 0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
METELEPHONE: (617) 542-8906
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Best Local Similarity 68.0°
Matches 1614; Conservative
                                                                                                                                                                                                        TELEX: 200154,
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9709
                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
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TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 778
                                                              ACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG
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                                                                AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCCGAGTGGGAGT
                                                                                       3736 AAACATGGGAAGCATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCCTGAGTGGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAINS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scully, Scott, Murphy & Presser 400 Garden City Plaza
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APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NOW-PATHOGENIC ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/388,353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08388353 Patent No. 6010895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 96(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                  Score 1100.4; DB 3 Pred. No. 1.7e-172;
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TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                Query Match
Best Local Similarity 68.0%;
Matches 1614; Conservative
                                                                          LENGTH: 9709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-388-353-1
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959 ACCCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGCGACGCCTACT
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                                                                                2776 ATTICAGAGAACTTAATAAGAGAACTCCAAGATTTCTGGGAAGTTCAATTAGGAATACCAC
                                                                                                                                    1019 TCAGCGTGCCCCTGGACGACGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA
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AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCG
                                                                                                                                                                                                                                                                                 TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGCCCCAGCCCGACAAAGAGCGAGAGGGG
                                                                                                                     2033 GCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGCAGA
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF INUMBER OF SEQUENCES: 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY STATE: NEW YORK COUNTRY: U.S.A. ZIP: 11530-0239 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk
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FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 08/388,353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
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COMPUTER: IBM PC compatible
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                                                                                                                                                 Length 9709;
                                                                                                                                              44.7%; Score 1100.4; DB 3; 68.0%; Pred. No. 1.7e-172; tive 0; Mismatches 736;
                           TYPE: nucleic acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               Conservative
                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-1
                                                                                                                                                                 Similarity
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Matches 1614;
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3916 GATATGTAACTGACAGAGGAAGAACAAAAAGTTGTCCCCCTAACGGACACAAATCAGA 3975
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TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
FILE REPRENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
EARLIER PAPLICATION NUMBER: DE 198 56 463
EARLIER PILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
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; Patent No. 6440730
; GENERAL INFORMATION:
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                                        ------CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGG
                                                                                         419 TGGGCGGCCAGATCAAGGAGGCCCTGCTGGAACCGGCGCCCGACGACGACGTGCTGGAGG
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3256 CTGATAAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAGGACAGCTGGACTGTCAATG 3315
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APPLICANT: CHANG,
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                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                 STREET: 624 Ninth Street, N.W. CITY: Washington STATE: D.C. COUNTRY.
   LENTIVIRAL VECTORS: 20
                                                                                                                                                                                                                                                                                 US/08/935,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = ""DNA""
                                                                                                                                                                                                                                                                                                 FILING DALL.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20,005
REFECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12494 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0)
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
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                                                                                                                                                 ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TITLE OF INVENTION: LE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Matches 1614; Conserv
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TOPOLOGY: Lir
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                                                       2567 ITTCAGTTCCCTTAGATAAAGACTTCAGGAAGTATACTGCATTTACCATACCTAGTATAA
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                                       539 AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG
                                                                                                                     599 IGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT
                                                                                                                                                                                                  659 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
                                                                                                                                                                                                                                                                              719 TGGACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAGATCAAGGCCCTGACCG
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                                                   AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1732
                                                                          3227 AATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAATATGCAA 3286
                                                                                                      AGATGCGCACCGCCCACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG 1792
                                                                                                                                                                      TCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG 1972
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IITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
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STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGGAAAGTACTATTTTAGATGGAATAGAT 3918
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MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
                                          APPLICATION NUMBER: US/08/848,760B
                                                                                                                                                                                                                        REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                       PRIOR APPLICATION DATA:

APPLICATION WUBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                               FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12494 base pairs TYPE: nucleic acid
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                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                        NAME: PACE, DORAN R.
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Matches 1614; Conservative
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San Francisco
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FILING DATE: No. 6027881 yet assigned
CLASSIFICATION: 435
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APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea
TITLE OF INVENTION: Proteins Having
NUMBER OF SEQUENCES: 37
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                               22; Gaps
                                                                                                                                                                                                                                                                                                                     AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG
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                                                                                                                                                                                                                                                                      Length 15581
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                  Score 1100.4; DB 3;
Pred. No. 1.8e-172;
0; Mismatches 736;
                                     015280-249000
                                                                                                                                                                                                                         ; OTHER INFORMATION: /note= "pNLnSG11"
US-08-646-538-35
                                 REFERENCE DOCKET NUMBER: 01528
TELECHMUNICATION INCORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 35:
SEQUENCE CHARACTERISTICS:
LEWSTH: 15581 base pairs
                         31,677
                                                                                                                                                                                                                                                                  44.78;
68.08;
ATTORNEY/AGENT INFORMATION:
         NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                           Matches 1614; Conservative
                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                           1..15581
                                                                                                                                                          linear
                                                                                                                                                                      MOLECULE TYPE: DNA
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                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                          TOPOLOGY:
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1493 TGCGCCAGCTGTGCAAGCTGCTGCGGGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGA 1552
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                                                                                         779 CCATCTGCGAGGAGATGGAGAAGGAGGCCAAGATCACCAAGATCGGCCCCGAGAACCCCT
                                                                                                                            2656 AAATTTGTACAGAAATGGAAAAGGAAAAATTTCAAAAATTGGCCTGAAAATCCAT
                                                                                                                                                                                                         839 ACAACACCCCCGTGTTCGCCATCAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG
                                                                                                                                                                                                                                              2716 ACAATACTCCCAGTATTGCCATAAAGAAAAAAGACAGTACTAAATGGGAAAATTAGTAG
                                                                                                                                                                                                                                                                                                                                  ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
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                                                                                                                                                                                                                                                          Length 15581;
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                                                                                                                                                                                                                                                                                        736; Indels
                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                        Score 1100.4; DB 4 Pred. No. 1.8e-172;
                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                          ; LOCATION: 1..15581
; OTHER INFORMATION: /note= "pNLnSG11"
US-09-503-222-35
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          44.7%;
68.0%;
                                                                                          LENGTH: 15581 base pairs
                                                                                                                                                                                                                                                                                      Matches 1614; Conservative
                                                                                                                          single
                                                                                                        nucleic acid
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                    MOLECULE TYPE: DNA
                                                                                                                                      linear
                                                                                                          TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                  NAME/KEY:
                                                                                                                                      TOPOLOGY:
                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                       TCAGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 1078
                                                                                                                                                                                                                                                           ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                              CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACG 1432
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                        2656 AAATTTGTACAGAAATGGAAAGGAAGGAAAATTTCAAAAATTGGGCCTGAAAATCCAT
                                                                ACCCCCCCCCCCGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT
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                                                   ACAACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG
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APPLICANT: BAIER, MICHAEL
APPLICANT: BAIER, MICHAEL
APPLICANT: BAIER, MICHAEL
APPLICANT: BAIER, MICHAEL
APPLICANT: WERNER, ALBRECHT
TITLE OF INVENTION: Upphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: UNBER: US/08/944,449
CURRENT APPLICATION NUMBER: EP 95113013.2
EARLIER FILING DATE: 1995-08-18
EARLIER FILING DATE: 1995-04-07
NUMBER OF SEQ ID NOS: 8
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GCGCCGAGACCTTCTACGTGGACGGCGCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
                                                                                                                                                                                                      GCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGA
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; ORGANISM: Human immunodeficiency virus type 1
US-08-944-449-7
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Matches 1608; Conservative
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2482 2542 2602 2662 1018 1078 2422 2722 3023 CACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAACAGAATC 3082 778 928 364 TTTCAGTTCCCTTAGATAAAGACTTTAGAAAGTATAACTATTAGCATTACCATACCTAGAATAAA 1944 TTAGGAACCAAAGAAAGACTGTTAAGTGTTTCAATTGTGGCAAAGAAGGGCACATAGCCA 2123 GGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACAGAAGAGAGC 2183 TTCAGGTTTGGGGAGGAGAAAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAA GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC TGCAGGTGCGCGCGCG-----ACAACCCCCGCAGCGAGGCCGGCGCGGCGCCAGGGCA AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCA AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG TATTAGTAGGACCTACACCTGTCAACATAGTTGGAAGAAATCTGTTGACTCAGATTGGTT GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCAGCTGAAGCTGAAGCCCGGCA TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG ACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG ATTICAGAGAACTTAATAAAAGAACTCAAGACTTCTGGGAAGTTCAGTTAGGAATACCAC ACCCCGCCGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA GCAACTGCCGCGCCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGA AAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAGATGTGGAAGGGAAGGACACCAAA TGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCGCGGAGGACCTGGCCTTCCCCCAGG GCAAGGCCCGCGGGAGTTCCCCAGCGGGAACCGCGCCAACAGCCCCACCAGCGCGAGC -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGG TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGG TGCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT CCATCTGCGAGGAGATGGAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT ACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC ACCCCGCAGGGTTAAAAAAAAAAAATCAGTAACAGTATTGGATGTGGGTGATGCATACT 2004 311 2243 419 2363 539 2423 2483 2543 719 2603 779 2723 2783 2843 2903 1079 2963 365 479 1019 131 599 629 839 959 1139 191 251 899 qq ò g g ò P δ g δ g ò qq Qγ g Ω a ò Q Ôχ Оþ οy QQ δ Q Qγ qq ò Q δ g ò g δý g δ a óλ

1492 1552 1612 1672 3622 3742 1912 1972 3922 4042 2212 4162 1733 AGATGCGCACCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAGATCG 1792 2032 3383 TAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGGTAATACCACTAA AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA TCGTGAACACCCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG --GGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG CTGATAAATGGACAGTACAGCCTATAATGCTGCCAGAAAAAAGACAGCTGGACTGTCAATG ACATACAGAAGTTAGTGGGAAAATTGAATTGGGCAAGTCAGATTTATGCAGGGATTAAAAG TGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCCAAGGCCCTGACCGACATCGTGCCCTGA CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGCGAGCCCGTGCACG 1613 GCGTGTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCAAGACC GCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCG GCTACGTGACCGACCGGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGA AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCG TAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGAATCAG GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGGGCTTCACCA CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC CACCAGACAAAAAACATCAGAAAGAACCTCCATTCCTTTGGATGGGTTATGAACTCCATC CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGGAGTGGGAGT CCGAGATCGTGATCTACCA---1853 1253 3143 1313 3203 3263 1433 1493 1553 3503 1673 3563 3743 1913 3803 1973 2033 3923 2093 3983 2153 1199 1373 3323 1793 3863 4043 qq g qq a a g qq Q q QΥ g ò q QY g ŏ g ΩÝ qq δy QQ QΥ q δ Qγ qq δy $^{\circ}$ δy QΥ δ g QΥ δy QΥ á

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2273 TGCCCGCCCACAAGGGCATCGGCGCAACGAGCAGTCGACAAGCTGGTGAGCAAGGGCA 2332
                         4163 TACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAA 4222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1944 TTAGGAACCAAAGAAAGACTGTTAAGTGTTTCAATTGTGGCAAAGAAGAGGGCACATAGCCA 2003
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                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30B (EPO)
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Pred. No. 6.5e-171;
0; Mismatches 742;
                                                    2333 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2364
                                                                  APPLICATION NUMBER: DE 195 13 152.
FILING DATE: 07-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 US/09/353,362
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    EP 95113013.2
                                                                                                                                              Sequence 7, Application US/09353362
Patent No. 6383739
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-353-362-7
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ilarity 67.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KLESNER, Sharon N. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 9737 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                     RESULT 15
US-09-353-362-7
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2123 GGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGAGC 2182
                                                                                                                                                                                                                                                                                                                                                                     2303 TAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAG 2362
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                                                            TGCAGGTGCGCGCG-----ACAACCCCCGCAGCGAGGCCGGCGCGAGCGCCAGGGCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2663 AGATATGTACAGAAATGGAAAAGGAAAGGAAAATTTTCAAAAATTGGGCCTGAAAATCCAT
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                                                                                               2783 ATTICAGAGAACITAATAAAAGAACITCAAGACTICIGGGAAGITCAGITAGGAATACCAC
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1373 CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAACG 1432
                                                                                                                                                       1913 TCGTGAACACCCCCCCCTGGTGAAGCTGTACCAGCTGGAGAAGAGCCCATCATCG 1972
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              1553 CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG
                                                                                                                                                                                                       2093 AGACCGAGCIGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGIGAACATCG
                                              3803 TIGICAAIACCCCTCCCTTAGTGAAATTATGGTACCAGTTAGAGAAACACATAGTAG
                                                                                                                   3383 TAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAA
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                                                                                                                                                                                                                                                                                      1733 AGATGCGCACCGCCCACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
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Search completed: February 10, 2003, 20:49:40 Job time : 149 secs

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February 10, 2003, 12:45:48; Search time 107.667 Seconds (without alignments) 10843.369 Million cell updates/sec
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1 gtcgacgccaccatggccga......gggctagcaccggtgaattc 2463
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GenCore version 5.1.3
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                                                                                                                                                                                                                              408267 seqs, 237001491 residues
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
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                                                                                                                                              Perfect score:
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                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | Segmence 2. Appli | | , - | Sequence 3. Appli | 1 | σ | · | | ì. | ì , | Segmence 3. Appli | 4 | Sequence 9. Appli | 4 | | ۸ | . 10 | Segmence 56, Appl | Sequence 56, Appl |
|---|--------------------------|-------------------|-----------------|-----------------|-------------------|-----------------|-----------------|------------------|------------------|-----------------|------------------|-------------------|-----------------|-------------------|-----------------|-----------------|-----------------|------------------|-------------------|-------------------|
| | ID | US-09-999-183-2 | US-09-872-733-6 | US-09-872-733-1 | US-09-872-733-3 | US-09-735-487-7 | US-09-735-487-9 | US-09-735-487-11 | US-09-735-487-13 | US-09-999-183-1 | US-09-737-190A-1 | US-09-943-286-3 | US-09-943-286-4 | US-09-943-286-9 | US-09-798-675-4 | US-09-798-675-5 | US-10-097-997-1 | US-09-886-156-56 | US-09-886-150-56 | US-09-886-149-56 |
| | Query Match Length DB | 4307 10 | 8366 10 | 4338 10 | 2467 10 | 2601 10 | 2601 10 | 2601 10 | 2601 10 | 4307 10 | 9719 10 | 8933 10 | 8933 10 | 8933 10 | 9544 10 | 9918 10 | 2348 9 | 9793 9 | 9793 9 | 9793 9 |
| ф | Query Match I | 66.3 | 63.6 | 62.1 | 47.3 | 44.9 | 44.9 | 44.9 | 44.9 | 44.9 | 44.9 | 42.8 | 42.8 | 42.8 | 42.5 | 42.5 | 34.3 | 33.7 | 33.7 | 33.7 |
| | Score | 1632.6 | 1566 | 1530.6 | 1163.8 | 1106.8 | 1106.8 | 1106.8 | 1106.8 | 1106.8 | 1106.8 | 1054.4 | 1054.4 | 1054.4 | 1048 | 1048 | 843.6 | 831 | 831 | 831 |
| | Result No. | , , , | 7 | m | 4 | ഹ | 9 | 7 | 8 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |

129 CCGCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCA 188

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189 GATGAAGGACTGCACGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCA 248

| Sequence 56, Appl. Sequence 14, Appl. Sequence 15, Appl. Sequence 5, Appl. Sequence 54, Appl. Sequence 1, Appl. Sequence 15, Appl. Sequence 15, Appl. Sequence 16, Appl. Sequence 17, Appl. | υ |); Length 4307; Indels 22; Gaps 5; TGATGCAGCGAGCAA 68 |
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| US-09-886-159-56 US-09-872-733-2 US-09-991-258-14 US-09-991-258-14 US-09-991-258-15 US-09-991-258-15 US-09-991-258-1 | ALIGNMENTS 183 ection Method 09/999,183 9 1800/02136 65.2 | tch |
| 20 831 33.7 9793 9 2 2 6 8 2 4 25.0 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | SULT 1 -09-999-183-2 Sadeuence 2, Application US Patent No. USZ0020147169A1 APPLICANT: MITROPHANOUS, TITLE OF INVENTION: In Vi- FILE REFERENCE: 674533-20 CURRENT APPLICATION NUMBE CURRENT APPLICATION NUMBER: PRIOR PRILNG DATE: 200 PRIOR PRILNG DATE: 1999-0 NUMBER OF SEQ ID NOS: 26 SOFTWARE: SeqWin99 SEQ ID NO 2 LENGTH: 4307 TYPE: DNA ORGANISM: Artificial SeqUERTINEM FEATURE: A37 TYPE: DNA ORGANISM: Artificial SequeRTINEM FEATURE: A37 TYPE: DNA ORGANISM: Artificial SeqUERTINEM FEATURE: A37 | Query Ma Best Loc Matches 12 1086 69 |
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1076 1016 2104 CAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAA 1196 1251 CGGCCAGCACCGCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCTGCGCGTTCAC 1310 1744 1804 1924 2044 1805 GATGGACGCCCGAAGGTCAAGCAATGGCCATTGACAGGGGGAGAAGATCAAGGCACTGGT 1864 1266 GATGAAAGACTGTACTGAGAGACAGGCTAA-TTTTTTAGGGAAGATCTGGCCTTCCTACA 1324 1505 GATAGGGGGGCAGCTCAAGGAGGCTCTCCTGGACACCGGAGCAGACGACACCGTGCTGGA 1564 1565 GGAGATGTCGTTGCCAGGCCGCTGGAAGCCGAAGATGATCGGGGGAATCGGCGGTTTCAT 1624 969 716 836 896 416 476 CCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTA 2045 GCACCCCGCAGGGCTGAAGAAGAAGAATCCGTGACCGTACTGGATGTGGGTGATGCCTA CTTCTCCGTTCCCCTGGACGACGACGAGGAGGTACACTGCCTTCACAATCCCTTCGAT CCCCGAGATCGTGATCTACCA-----GGCCCCCCTGTACGTGGGCAGCGACCTGGAGAT 477 GGAGATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGATCGGCGGCATCGGCGGCTTCAT 537 CAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCCAAGAAGGCCATCGGCAC CTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGG 1745 TTGCACGCTGAACTTCCCCATTAGCCCTATCGAGACGGTACCGGTGAAGCTGAAGCCCGG CATGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGAC 837 CTACAACACCCCCGTGTTCGCCATCAAGAAGGACAGCACCCAAGTGGCGCAAGCTGGT GTACAACACGCCGGTGTTCGCAATCAAGAAGAAGGACTCGACGAAATGGCGCAAGCTGGT GGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCC CTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCAT CAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGG 249 GGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGA CGTGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGG CGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCC GCTGCAGGTGCGCGG-----CGACAACCCCCGCAGCGAGGCCGGCGCGCGAGCGCCAAGGG CA-----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAA GGTGGGCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGA 309 1625 657 717 177 1925 1985 1017 2105 1077 2165 2225 1197 897 957 417 597 1137 2285 363 g ò Op qq g ò g pp ò g ŏ QQ ò g ö d ŏ g ολ qq ò g δ g Ω P Qγ g ò g ò g QY δ δ

1610 1790 1910 1970 2270 1430 1490 2150 2704 1611 CGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGA 1670 2764 2824 2464 2524 CGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTAACCTGAGCTG 2271 GGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGG 2465 CCCTGACAAAATGGACCGTGCAGCCTATCGTGCTGCCGCAGAGAAAAAAACAGCTGGACTGTCAA 2885 CACCACCGAAAGCATCGTGATCTGGGGAAAGACTCCTAAGTTCAAGCTGCCCATCCAGAA 1911 GTICGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCAT GAAGACTGAGCTGCAGGCCATTTACCTCGCTTTGCAGGACTCGGGCCTGGAGGTGAACAT CGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAG 1311 CACCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCA 2645 AACCGAGGAGGCCGAGCTCGAACTGGCAGAAAACCGAGAGATCCTAAAGGAGCCCGTGCA CGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAA GGAGACCTGGGAGCCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGA 3005 GITCGTCAACACCCCTCCCCTGGTGAAGCTGTGGTACCAGCTGGAAGAAGAAGTCATAGT 1971 CGGCGCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGC CCCCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGGTGGACCGTGAA CGACATACAGAAGCTGGTGGGGAAGTTGAACTGGGCCAGTCAGATTTACCCAGGGATTAA 1491 GGTGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCT GACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGGCCCGTGCA 2705 CGGCGTGTATGTATGACCCCTCCAAGGACCTGATCGCCGAGATCCAGAAGCAGGGCCAAGG 1671 CCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGC CAAGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGAT CATCCGCAAGGTGCTGTTCCTGGACGGCATCGA 2363 3245 2211 2525 1551 2765 2825 1791 1851 2031 3125 2091 2151 3305 3365 1371 1731 3185 2331 qq g δ g g δλ qq δy a qq δ g QΥ QQ ò g δy ōλ δy g qq g Qγ g δλ g οy Db ŏ g δ Qγ ò δ

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Sequence 6, Application US/09872733
GENERAL INFORMATION:
TELE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND TITLE OF INVENTION: SIV BWN GENES
TITLE OF INVENTION: SIV BWN GENES
TITLE OF INVENTION: SIV BWN GENES
TITLE OF INVENTION: SOLO 4287011 HIV GAG/POL, SIV GAG & ENV CURRENT APPLICATION NUMBER: US/09/872,733
FILE REFERENCE: 2001-06-01
PRIOR APPLICATION NUMBER: C001-06-01
PRIOR APPLICATION NUMBER: 60/173,036
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEC ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: DNA sequence OTHER INFORMATION: of the construct pCMVgagpolBNKan containing a CMV OTHER INFORMATION: promoter, a HIV gag/pol gene and a kanamycin OTHER INFORMATION: resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2037 TGAAAGATTGTACTGAGAGAGAGGCTAA-TTTTTAGGGAAGATCTGGCCTTCCTACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8366;
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Pred. No. 5.6e-252;
0; Mismatches 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.6%;
Best Local Similarity 80.3%;
Matches 1905; Conservative
                                                                                                                                                                                                                                                                                   SEQ ID NO 6
LENGTH: 8366
RESULT 2
US-09-872-733-6
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                                                               2696 ACAACACTCCAGTCTTCGCAATCAAGAAGAAGACAGTACCAAGTGGAGAAAGCTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                 599 TGCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT
                                                  659 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
                                                                                                                                                                                                                                                              ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
                                                                                                                                                                                                                                                                                                                 ACCCCGCCGGCCTGAAGAAGAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT
                                                                                                                                                                                                                                                                                                                             ACAACGAGACACCCAGGCATCCGCTACCAGTACAACGTGCTGCCACAGGGATGGAAGGGAT
                                                                                                    719 TGGACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG
                                                                                                                                                        779 CCATCTGCGAGGAGATGGAGAAGGAGGCCAAGATCACCAAGATCGGCCCCGGAGAACCCCT
                                                                                                                                                                                                         839 ACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG
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APPLICANT: The Government of the United States of America, as TITLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND TITLE OF INVENTION: SIV ENV GENES FILE REFERENCE: 2026-4287US1 HIV GAG/POL, SIV GAG & ENV CURRENT APPLICATION NUMBER: 05/09/872,733
PRIOR PLLING DATE: 2000-1-66-01
PRIOR APPLICATION NUMBER: PCT/USO0/34985
PRIOR FILING DATE: 2000-1-22
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
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                                                                                                                                                                                               3656 CCACAGAGAGCATCGTGATCTGGGGCAAGACTCCCAAGTTCAAGCTGCCCATACAGAAGG 3715
                                                                                                            3596 GGATGAGGGGTGCCCACACCAACGATGTGAAGCAGCTGACAGAGGCAGTGCAGAAGATCA 3655
                                                                                                                                                    1793 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1852
                                                                                                                                                                                                                                        1853 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGGAGT 1912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2033 GCTACGTGACCGGACCGGGCGGCGGAAGATCGTGAGCCTGACCGAGACCACCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                 1973 GCGCCGAGACCTTCTACGTGGACGCCGCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
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                                                                 1733 AGATGCGCACCGCCCACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
                                                                                                                                                                             Sequence 1, Application US/09872733 Patent No. US20010036655A1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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 Length 4338;
Score 1530.6; DB 10; Lengt
Pred. No. 4e-246;
0; Mismatches 444; Indels
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80.1%;
                 Best_Local Similarity 80.1
Matches 1905; Conservative
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                                                                                                          GGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGGGCCCGC 1194
                                                                  2464 GCATCCTGACAAGTGGACAGTGCAGCCCATCGTGCTGCTGAGAAGGACAGCTGGACTGT
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                                                     ATCAACAACGAGACCCCCGGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAG
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Sequence 3, Application US/09872733
Fatent No. US20010036655A1
GENERAL INFORMATION:
TGENERAL INFORMATION:
TILLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND
TITLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND
TITLE OF INVENTION: SIV ENV GENES
TITLE OF INVENTION: SIV ENV GENES
TITLE OF INVENTION: SIV ENV GENES
CURRENT APPLICATION NUMBER: US/09/872,733
FRIOR APPLICATION NUMBER: QC1/US00/34985
PRIOR APPLICATION NUMBER: 60/173,036
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 19
SOFWWARE: PATEURITY OF SEQ ID NOS: 19
SOFWWARE: PATEURITY OF SEQ ID NOS: 19
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ORGANISM: Artificial Sequence
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          TTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTG
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Sequence 7, Application US/09735487

Patent No. US2002004267941

GENERAL INFORMATION:
APPLICANT: HERTOGS, Kurt
APPLICANT: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
ITILE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION NUMBER: US/09/735,487

CURRENT FILING DATE: 2000-12-14

PRIOR FILING DATE: 1998-07-24

NUMBER: OF SEQ. ID NOS: 15
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68.2%; Pred. No. 8.7e-176;
ive 0; Mismatches 732; Indels
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COTHER INFORMATION: gag Polyprotein US-09-735-487-7
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Matches 1618; Conservative
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SEQ ID NO 7
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APPLICANT: GE BETHONE, Marie-Pierre
APPLICANT: HERTOGS, Kurt
APPLICANT: HERTOGS, Kurt
APPLICANT: PAUWELS, Rudi
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: HIV POSITIIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REPERENCE: 1377-1259
CURRENT APPLICATION NUMBER: US/09/735,487
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Patent No. US20020042679A1
GENERAL INFORMATION:
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                        TAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAG
                                                             AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG
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          PRIOR APPLICATION NUMBER: 09/117,217 PRIOR FILING DATE: 1998-07-24
                                                                                                                                      ; LOCATION: (334)...(489)
; OTHER INFORMATION: gag P6 (52 AA)
US-09-735-487-9
CURRENT FILING DATE: 2000-12-14
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                                    NUMBER OF SEQ ID NOS:
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                                                    ACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG
                                                                                                          916 ACAATACTCCAGTATTGCCATAAAGAAAAAAGACAGTACTAAATGGAGAAAATTAGTAG
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APPLICANT: HERDGS, Kutt
APPLICANT: PAUWELS, Rudi
TITLE OF INVENTION: WETHOO OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: OF HUMAN HIV STRAINS
TITLE OF INVENTION: OF HUMAN HIV STRAINS
CURRENT APPLICATION NUMBER: US/09/735,487.
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
NUMBER OF SCD ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
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              1996 TIGTTAATACCCCTCCCTTAGTGAAATTATGGTACCAGTTAGAGAAGAAGAACCCTTAGTGAA
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Pred. No. 8.7e-176;
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68.2%;
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; OTHER INFORMATION: Protease
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Best Local Similarity 68.2
Matches 1618; Conservative
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GCAACTGCCGCCCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGA 190
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                        -----CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGG
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APPLICANT: de BETH
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US-09-735-487-13
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                  CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACC
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Best Local Similarity 68.2%; Pred. No. 8.7e-176;
Matches 1618; Conservative 0; Mismatches 732;
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TITLE OF INVENTION: METHOD OF MANNESS.

TITLE OF INVENTION: HIV POSTITIVE BASED ON T

TITLE OF INVENTION: OF HUMAN HIV STRAINS

FILE REFERENCE: 1377-125P

CURRENT APPLICATION NUMBER: US/09/735,487

CURRENT FILING DATE: 2000-12-14

FILING DATE: 1998-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (750)..(2435)
; OTHER INFORMATION: Reverse Transcriptase
US-09-735-487-13
                                                                                                     de BETHUNE, Marie-Pierre
HERTOGS, Kurt
                                                                                                                                                                                                                                               Sequence 13, Application US/09735487 Patent No. US20020042679A1
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Tue Feb 11

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Patent No. US20020147169A1
GENERAL INFORMATION:
TELENCANT: MITROPHANOUS, et al
TITLE OF INVENTION: In Vivo Selection Method
FILE REPERENCE: 67452-2009
CURRENT APPLICATION NUMBER: US/09/999,183
CURRENT FILING DATE: 2001-11-29
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1909-06-03
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: SeqWin99
SEQ ID NOS: 26
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                                                     Length 4307
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                                                    44.9%; Score 1106.8; DB 10; 68.2%; Pred. No. 8.9e-176;
        ORGANISM: Human immunodeficiency virus type I
                                                  Query Match
Best Local Similarity 68.29
Matches 1618; Conservative
                     US-09-999-183-1
TYPE: DNA
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APPLICANT: Shibuya, Tetsuo
TITLE OF INVENTION:
APPLICANT: Shibuya, Tetsuo
TITLE OF INVENTION: A Method for Changing a Target Array, a Method for Analyzing
TITLE OF INVENTION: A Structure, and an Apparatus, a Storage Medium and a
TITLE OF INVENTION: Taransission Medium Therefor
TITLE OF INVENTION: Taransission Medium Therefor
CURRENT APPLICATION NUMBER: US/09/737,190A
CURRENT FILING DATE: 2000-12-14
SUMMER OF SEQ ID NOS: 2
SOFTWARR: Patentin Ver: 2.1
SEQ ID NO 1.2.
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Matches 1618; Conservative
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                                                                                                                                                                                                                            2236 CTGTATCCTTTAACTTCCCTCAGGTCACTCTTTGGCAACGACCCCTCGTCACAATAAAGA 2295
                                                         419 TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCGCGACGACGACACCGTGCTGGAGG 478
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 TGCGCCAGCTGTGCAAGCTGCTGCGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCTGA 1552
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                                                                      CCGAGGAGGCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG
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APPLICANT: NUNDMUTA, KIDOTADA
TILE OF INVENTION: POLINUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02.UT
CURRENT APPLICATION NUMBER: US/09/943,286
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 9
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Patent No. US20020106668A1
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                                                                                                                                                 transcripts produced from the BH10
                                                                                                                                                                                                                     Query Match 42.8%; Score 1054.4; DB 10; Length 8933; Best Local Similarity 55.4%; Pred. No. 4.6e-167; Matches 1335; Conservative 279; Mismatches 736; Indels 58;
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                                                    TYPE: RNA
ORGANISM: Human Immunodeficiency Virus
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                                                                                                                                               of
                                                                                                                            LOCATION: (1)...(8933)
OTHER INFORMATION: Sequence
OTHER INFORMATION: plasmid.
                                                                                                           NAME/KEY: source
                                   LENGTH: 8933
                                                                                                                                                                                 US-09-943-286-3
                  SEQ ID NO 3
                                                                                          FEATURE:
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LOCATION: (4135)...(4155)
OTHER INFORMATION: Mutated positions: 4135, 4140-1, 4145,
OTHER INFORMATION: 4152-3, 4155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nunomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REPERENCE: 9D104-02.UT
CURRENT APPLICATION NUMBER: US/09/943,286
CURRENT FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09943286 Patent No. US20020106668A1 GENERAL INFORMATION:
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SOFTWARE PARKED for Windows Variety In No. 1
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (4140) ...(4159)
OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152
OTHER INFORMATION: 4156-57, 4159
                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Sequence of the IAC-Bscr pseudo target
                                                                                                                                                                                                                      APPLICANT: Nunomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02.UT US/09/943,286
CURRENT APPLICATION NUMBER: US/09/943,286
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                           Sequence 9, Application US/09943286
Patent No. US20020106668A1
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ORGANISM: Artificial Sequence
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                                                                                        CCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGT
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TITLE OF INVENTION: HIV VACCINES
TILE REFERENCE: E056 2020
CURRENT APPLICATION NUMBER: US/09/798,675
CURRENT FILING DATE: 2001-12-11
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PRIOR FLING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/251,083
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
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Patent No. US20020106798A1
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US-09-798-675-4
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OTHER INFORMATION: Construct of vaccine vector pGA2 and insert JS2 expressing cla
                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1401)..(3617)
OTHER INFORMATION: encoding viral rproteins including reverse transcriptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9544;
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                                                                                                                                                                                                                 high level of virus particles
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1048; DB 10;
Pred. No. 5.3e-166;
0; Mismatches 740;
                                                                                     LOCATION: (106)..(1641)
OTHER INFORMATION: encoding inner core protein
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
; LOCATION: (6672)..(9544)
; CTHER INFORMATION: Vaccine vector pGA2
08-09-798-675-4
                                                                                                                                                                                                                                                                                                                               Env
                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (4102)..(6660)
OTHER INFORMATION: encoding ADA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.5%;
Best Local Similarity 66.9%;
Matches 1610; Conservative
                                                   OTHER INFORMATION: HIV-1 VL
                                                                                                                                                                                              LUCATION: (3708)...(6334)
OTHER INFORMATION: induces
NAME/KEY: misc feature
                                                                                                                                                                                                                                                     LOCATION: (3847)..(6518)
OTHER INFORMATION: encodes
                                                                                                                                                                             NAME/KEY: misc-feature LOCATION: (3708)..(6334
                                                                       NAME/KEY: misc_feature
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                       2932 AGCCATTTAAAAATCTGAAAACAGGAAAATATGCAAGAATGAGGGGTGCCCACACTAATG
                                                                 AGCTGTGGTACCAGCTGGAGAAGGAGCCCATCGGCGCCCGAGACCTTCTACGTGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HTV VACCINES
FILE REFERENCE: E056 2020
CURRENT APPLICATION NUMBER: US/09/798,675
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 24
SOUTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/09798675; Patent No. US20020106798A1; GENERAL INFORMATION:
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OTHER INFORMATION: Construct of vaccine vector pGA1 and vaccine insert expressing OTHER INFORMATION: ade B HIV-1 Gag-Po

TYPE: DNA ORGANISM: Artificial Sequence

LENGIH:

FEATURE:

NAME/KEY: misc_feature

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                                                           NAME/KEY: misc_feature
LOCATION: (3708)..(5715)

OTHER INFORMATION: regulates high-level production of HIV genes
LOCATION: (3847)..(5944)

OTHER INFORMATION: encodes protein regulating the transfer of RNA to cytoplasm
NAME/KEY: misc_feature
LOCATION: (3939)..(4181)

OTHER INFORMATION: gene participates in viral assembly and budding
NAME/KEY: misc_feature
LOCATION: (4099)..(4041)

OTHER INFORMATION: encodes truncated form of viral coat protein
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OTHER INFORMATION: encodes proteins of viral inner core MAME/KET: misc_feature LOCATION: (1401) (1401) OTHER INFORMATION: encodes viral proteins but not integrase
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                                                                                                                                                                                                                                                                                                                                      42.5%; Score 1048; DB 10; 66.9%; Pred. No. 5.3e-166;
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LOCATION: (6098)..(9918)
OTHER INFORMATION: vaccine vector pGA1
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Matches 1610; Conservative
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CCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGT
                                                                                          GGCCCCTGACCGAGGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGG
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                                 1817 GCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCG
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zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensburg,E.
Polynucleotides encoding antigenic hiv type c polypeptides,
polypeptides and uses thereof
Patent: WO 0204493-A 32 17-JAN-2002;

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| ALIGNMENTS AX455916 Sequence 32 from Patent WO0204493. AX455916 AX455916 AX455916 AX455916 Synthetic construct. Synthetic construct artificial sequences. | +10 | 9.0 | 50.1 | 01 | | AF110974 AF110975 | AFII AFII | HIV-1 is |
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| AX455916 2457 bp DNA linear PAT 06 Sequence 32 from Patent W00204493. AX455916 AX455916 I GI:21714901 Synthetic construct. Synthetic construct artificial sequences. | RESULT 1 | | | | | | | |
| Sequence 32 from Patent W0020449 AX455916.1 GI:21714901 Synthetic construct. Synthetic construct artificial sequences. | AX455916 LOCUS | AX4 | | | | α. | 7 | 90 |
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| Qy 2395 TACGTGGCAGGGG Db 2401 TACGTGGCAGCGG QY 2455 TTC 2457 Db 2461 TTC 2463 | RESULT 3 AX455914 LOCUS DEFINITION Sequence 30 ACCESSION AX455914 VERSION AX455914 KEYWORDS SOURCE SYNTHETIC CO ORGANISM SYNTHETIC CO | AUTHORS ZUR Megede,J TITLE POLYNUCLEOETI POLYPETIGES JOURNAL PATENT WO O FEATURES LOC SOURCE LOC SOURCE LOC AND SOURCE LOCALIZED LO | Query Match Best Local Similarity Matches 2451; Conserv | Oy 1 GTCGACGCCACT | Oy 61 CGCAGCAACTTCAAN | Db 121 CACATCGCCCGCAAA Qy 181 GGCCACCAGAATGAAA Db 181 GGCCACCAGATGAAA DB 181 GGCCACCAGATGAAAAAAAAAAAAAAAAAAAAAAAAAAA | Qy 241 TTCCCCAGGGCAN | Db 301 AGCGGGAGCTGCA Qy 361 GGCACCTGAACTT Db 361 GGCACCTGAACTT | Oy 421 GGCGCCAGATCAA |
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| 1261 CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGGCTTCACCACCCCCGAC 1320 1321 AAGAAGCACCCCGAAGGAGCCCCCCTTCCTGCCCAAGTTCGAGCTGCACCCGACAAG 1374 | 1435 AAGCTGGTGGGCAACCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCCCAG | 1615 TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACC 167 | 1795 AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGAGAGACCTGG 1854 | 1855 GAGACCTGGTGGACCGACTACTGGCAGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1914 | 1915 AC 1921 AC 1975 AC | 1981 ACCTTCTACGGGCGCGCCGCCAACCGGGAGACCAAGATCGGCAAGGCCGGCTACGTG 2040 2035 ACCGACCGGCGGAGAAGATCGTGAGCCTGACCAGAGACCAACAACAACAACAGAGCCGGC 2041 ACCGACCGGGCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGAAGACCGAG 2094 2041 ACCGACCGGGGCCGGCAGAAGATCGTGAGCCTGACCACAACCACAACAACCGAAGACCGAG 2100 | 2095 CTGCAGGCCATCCAGCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGAC | 2161 2215 2221 | 2275 CACAAGGCATCGGCGACAACGAGTCGACAAGCTGGTGAGCAAGGCATCCGCAAG 2334 |
| 90 Ay 40 | \(\delta \) \(\d | 90 00 00 00 00 00 00 00 00 00 00 00 00 0 | da Op | Qy Dp | QY Db QY | qa qa | oy oy | do do | da Vo |

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GGGGCCCTAGGATCGATTAAAGCTTCCCGGGGCTAGCACCGGTGAA 2454
                                                                                                                                                                                                                                                                                     J., Barnett, S.W., Engelbrecht, S. and van Rensburg, E. .: des encoding antigenic hiv type c polypeptides, se and uses thereof 0204493-A 30 17-AAN-2002; ORRATION (US); University of Stellenbosch (ZA)
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| GGGCCAGTACGACCAGATCCTGACATCTGCGGCAAGAAGGCCATCGGCACCGT | CTGATCGGCCCCACCCCGTGAACATCGCCCGCAACATGCTGACCCAGCTGGCTG | ACCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAACCTGAAGCCGGCATG | GACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCCTTIIIIIIIIII | ATCTGCGAGGAGATGGAGAGGGAAGATCACCAASATCGGCCCGGAGAACCCCTAC | AACACCCCGTGTTCGCCATCAAGAAGAAGACACCACCAAGTGGCGCAAGCTGGTGGCCCCTIIIIIIIIII | TTCCGCGAGCTGAACAAGCGCACCCAGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC | CCCGCCGCCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGCGACGCCTACTTC | AGGIGGCCCTGGACGAGGACTICCGCAAGTACACGCCTTCACCATCCCCAGCATCAACHHHHHHHHHH | AAGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCAGC | CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCC | GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCACCTGGACCTGGAGTTCGC | CAGCACCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACCIIIIIIIIII | CCCGACAAGAAGCACCAGAAGGACCCCCTTCCTGCCCATCGAGCTGCACCCCIIIIIIIIIIIIIIIIIIIIIIIIIII | GACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGGCTGGACCGTGAACGACTGCTTTTTTTT | ATCCAGAAGCTGGTGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTG | CGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCTGACC | GAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGC |
| 4 4 | 601 | 661 | 721 | 781 | 841 | 901 | 961 961 | 1021 | 1081 | 1141 | 1201 | 1255 | 1315 | 1369 | 1429 | 1489 | 1549 |
| Qy Db | QY Db | Qy | QY | Qy | Qy | Qy | Qy Db | Qy | QY Dp | Qy Db | Qy Db | Qy Db | Qy Db | Qy Db | Qy Db | Qy | Qy |

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1609 GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAG 1668
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                1621 GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGAG
                                                                            1681 TGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGGAAGTACGCCAAG
                                                                                                                                            1801 ATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAG
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                                                            1669 TGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG
                                                                                                                       1729 ATGCGCACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCC
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Pred. No. 1e-200;
0; Mismatches 182; Indels
                                                                                                     HIV
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Modifications of hiv env, gag, and pol
genetic immunization
Patent: WO 0233943-A 168 25-APR-2002;
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                                                                                            AGGTGCGCGG ----CGACAACCCCCGCAGCGAGGCGGCGCGGGGCGCCAGGGCA---
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| RESULT 6 AX427931 LOCUS DOCUS DEFINITION ACCESSION VERSION KEEWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE SOURCE | ORIGIN ORIGIN Querty Mathematics Matches 2 Qy 14 Tr Ob 2967 Tr Oy 74 Av Ob 3027 Av | Oy 134 A Db 3084 A OY 194 A OY 254 A OY 254 A OY 3503 A Db 3203 A | Qy 365 - Qy 422 G Qy 422 G Qy 482 T Qy 482 T Qy 602 T Qy |
|--|---|--|---|
| 1316 CCGACAAGAAGCACCAGAAGGAGCCCCCTTCGTGCCCATCGAGCTGCACCCCG 1369 | 4575 1670 4635 1730 4695 1790 | OY 1850 CCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCGAGTGGGAGTTCG 1909 4815 [111111111111111111111111111111111111 | 0y 2090 CCGAGCTGCAGCCATCCAGCTGCAGGACAGGGGGGGGGG |
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PAT 20-JUN-2002
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0.212943-A 169 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGCCGCGCCCTGCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGCCCACCAGATGA 3143
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/db_xref="taxon:32630"
/nte="plasmid pVR1012x/s containing HIV genes"
a 2668 c 2505 g 1769 t
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 linear
 DNA
AX427931 9169 bp 1
Sequence 169 from Patent WO0232943.
                                                         AX427931.1 GI:21538018
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synthetic construct
artificial sequences.
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2178; Conservative
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| 721 3682 781 3742 841 | 901 3862 961 3922 | 102 398: 108: | 4 0 0 | 4162 1255 4222 | T 8 | 136 | 1429 | 1489 4462 | 1549 4522 | 1609 4582 | 1669 4642 | 1729 4702 | 1789 |
|--|---|-------------------------------------|----------|---|---|---|--------------|--|--|---|---|--|--|
| CCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCAAGCTGAAGCCGGCATGG [| ACACCCCGTGTTCGCCATCAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGACT | 114 1 1 1 1 1 1 1 1 | 38 – S | :ATCTTCCAGTGCAGCATGACCAAGATCCTGGAGCCCTTCCGCAAGCAGAACCCC GTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGC | GCACCGCCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCAC | AGAAGCACCAGAAGGACCCCCTTCCTGCCCATCGACAGAAGCACCATCAAGAAGCACCCCTTCCTGTGGATGGCTACGAAGGAGCCCCCTTCCTGTGGATGGGCTACGA | ACCGTGCA | TCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCAATCTACCCCGGCATCAAGGTGC | GCCAGCTGTGCAAGCTGCTGCGGGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCG | AGGAGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCG | TGTACTACGACCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGT | GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGGCAAGTACGCCAAGA | TGCGCACCGCCACCACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA |
| 662 3623 722 3683 782 3743 | 842 3803 902 3863 | 962 3923 1022 3983 | 04 04 | 0 0 | 5 2 2 | - ∞ : | 4 | 1430 | 1490 | 1550 | 1610 | 1670 | 1730 |
| 60 A A A A A A A A A A A A A A A A A A A | oy Oy | Qy Db Oy | QY Db | Oy Dp | oy da | 5 a 6 | qq Dp | Qy Db | QY | Oy Db | QY | Qy | οy |

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PAT 20-JUN-2002
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0232943-A 164 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
1. 9194
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4703 TGAAGGGGCCCACACCACCACGAGGTGAAGCAGCTGACGAGGGCCGTGCAGAAGATGGCCA 4762
                                                                                               1850 CCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG 1909
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                                                      4763 CCGAGAGCATCGTGATCTGGGCCAAGACCCCCAAGTTCAAGCTGCCCATCCAGAAGGAGA
                                                                                                            1970 CCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGCT
                                                                                                                                                                                                                      2090 CCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGA
                                                                                                                                                                                                                                                                                                                                  5063 CCGAGCTGCAGGCCATCCACCTGCACGCACCTGCAGGCCTGGAGGTGAACATCGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/db_xref="taxon:32630"
/note="plasmid pVR1012x/s containing HIV
1 2672 c 2523 g 1767 t
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AX427926.1 GI:21538013
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artificial sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5303
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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| qa | 111 2967 TGG | | 3026 |
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| Qy Db | 71 TCA 3027 TCC | CAAGGCCCCAAGCGCATCATCAACTTCAACTGCGGCAAGGAGGCCACATCGCCC : | 130 3086 |
| Oy Db | 131 GCA 3087 GCA | CAACTGCCGCCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGGAGGCCCACCAGA : | 190 3146 |
| Qy Db | 191 TGA 3147 TGA | GAAGGACTGCACCGACGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG | 250 3205 |
| QY da | 251 GCP | GCAAGGCCGGCGAGTTCCCCAGCGAGCAGAACGGCGCCAACAGCCCCACCAGCGCGGGAGC | 310 |
| 3 | 311 T 356 T 256 T | GCAGGTGCGCGGCGACAACCCCGCGGGGCCGGGGGCGCAGGGCAALING | 32 |
| Q7 Oy | 365 | cccrgaactrccccagarcaccrgragagcagcgcccrggragagagcarcaagg crgaarcarcarraaga | 418 3385 |
| op Op | 419 TGC 3386 TAC | GGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCGACGACGACGACGACGAGGAGGAGAAGA | 478 3445 |
| Qy Db | 479 AGE 3446 AGE | AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGATGATCGGCGGCGTGCCGGCGGCTTCATCA | 538 3505 |
| ζς Op | 539 AGC 111 3506 AGC | AGGIGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG | 598 3565 |
| oy Ob | 599 TGC 3566 TGC | GCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGGCT | 658 3625 |
| Qy Db | 659 GCZ 3626 GCZ | GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCGGCA | 718 3685 |
| oy Db | 719 TGC 3686 TGC | GGACGGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG | 778 3745 |
| Oy Db | 779 CC | CCATCTGCGAGGAGATGGAGAAGGAGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT | 838 3805 |
| Qy Db | 839 AC | ACAACACCCCCGTGTTCGCCATCAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG | 898 3865 |
| Qy Db | 899 AC | ACTICGGGAGCTGAACAAGGCACCCAGGACTICTGGGAGGTGCAGGTGGGCATCCCCC | 958 3925 |
| Qy | 959 ACC 11 3926 ACC | ACCCGCCGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT | 1018 3985 |
| λ G | 1019 TC | CAGGGGCCCCTGGACGAGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA | 1078 |
| δy | 1079 AC | ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA | 1138 |

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4046 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA 4105
                                                                                                                                                                                1313 CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCAT-----CGAGCTGCACC 1366
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                         4226 GCCAGCACCGCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGCGCTGGGGCTTCACCA
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                                                                            CCGAGATCGTGATCTACCA-----GGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG
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| 7 AGCTGGTGAACCAGATCATCAAGCAGAAGGAGAAGGTGTACCTGAGCTGGG 2266 | AX427925 Sequence 163 from Patent W00232943. AX427925 AX427925 AX427925 AX427925. Granthetic construct. Synthetic construct. Coverion (1) 10 10 4 10 10 10 10 10 10 10 10 10 10 10 10 10 | Duery Match Bo.3%; Score 1973.4; DB 6; Length 9194; Bast Local Similarity 90.9%; Pred. No. 7.6e-198; Indels 28; Gaps 6; Batches 2176; Conservative 0; Mismatches 191; Indels 28; Gaps 6; 14 TGGCCGAGGCCATGAGCCAGGCACCAGGCCAACATCCTGATCCAGCGAGCAACT 70 |
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| 2207 1 5186 2 2267 3 5246 3 2327 5 | RESULT 8 AX427925 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL FEATURES SOUICE BASE COUNT | Ouery Match Best Local 14 TGG 11 TGA 2967 TGG 71 TCA 1307 TCA 1307 GCA 131 TGA 3206 GGA 311 TGA 3206 GGA 311 TGA 316 TGA 316 TGA 316 TGA 316 TGA 317 TGA 317 TGA 318 TGG 336 TTG 336 TTG 337 T |
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                                 AGGTGCGCCAGTACGACCAGATCCTGAGATCTGCGGCAAGAAGGCCATCGGCACCG
                                                                 TGCTGATCGGCCCCACCCCGGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT
                                                                          GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
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Location/Qualifiers

FEATURES

9

| 1606 | 1666 4645 | 1726 | 1786 4765 | 1846 4825 | 1906 4885 | 1966 4945 | 2026 | 2086 5065 | 2146 5125 | 2206 5185 | 2266 5245 | 2326 5305 | |
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| 7 CCGAGGAGGCCGAGCTGGCCCGAGAACCGCGAGATCCTGCGCGCGAGCCCGTGCACGCGTGCACGCGTGCACGCGTGCACGCGCGGAGCCCGTGCAGCCGTGCAGCCCGTGCACGCGAGGAGCCCGTGAAGCGCCGAGGAGCCCGTGCACGAGGAGCCCGTGAAGCACCGCGAGAACCGCGAGAACCGCGAGAACCGCGAGAACCGCGAGAACCGCGAGAACCGCGAGAACCGCGAGAACCGCGAGAACCGAGAACCGCGAGAACCAGAACCAGAACCAGAACCGAGAACCAGAACCGCGAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAGAACCAACACACACACACACACACACACACACACACACACA | GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGCCCACGACC | * AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA | 7 AGATGCGCACCGCCACCAACGACGACGAGCAGCTGACCGAGGCCGTGCAAGAAGTCG | 7 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAGG | 7 AGACCTGGGAGACCTGGTGCACCGACTACTGCAGGCCACCTGGATCCCCGAGTGGGAGT | 7 TCGTGAACACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGAAGAGCCCATCATCG | 7 GCGCCGAGACCTTCTACGTGGACGGCGCCCCAACCGCGAGACCAAGATCGGCAAGGGCG | 7 GCTACGTGACCGAGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAACAGA | 7 AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACGGCGGCGGCGGGGGGAGGTGAACATCG | 7 TGACCGACAGCAGTAGGCCCTGGGCATCATCCAGGCCCAGGCCGAGAAGAGGGAGCG | 7 AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG | 7 TGCCCGCCCACAAGGCCATCGGCGGCAACGAGCAGATCGACAAGGTGGTGAGCAAGGGCAALIIIIIIIIIIIIIIIIIIIIIIIIIII | 7 TCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTA 2381 |
| 1547 | 1607 | 1667 | 1727 4706 | 1787 | 1847 | 1907 | 1967 4946 | 2027 | 2087 | 2147 | 2207 5186 | 2267 5246 | 2327 |
| Oy Dp | QY | Qy Db | Qy Dp | Oy Dp | Qy | Qy Dp | Qy | Qy | Oy Dp | Qy Dp | Qy | Qy | Qy Db |

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                                                                                          Length 12411;
                                       /note="plasmid pVR1012x/s containing HIV genes" 3733 c 3476 g 2264 t
                                                                                                                     28;
                                                                                         Score 1973.4; DB 6; Length
Pred. No. 7.1e-198;
0; Mismatches 191; Indels

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    /organism="synthetic construct"
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Matches 2176; Conservative
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PAT 20-JUN-2002

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AX427927

DEFINITION

RESULT 9 AX427927 LOCUS ACCESSION VERSION

KEYWORDS

Sequence 165 from Patent W00232943. AX427927 AX427927.1 GI:21538014

synthetic construct. synthetic construct artificial sequences.

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

enhance immunogenicity for

Huang,Y. and Nabel,G.J.
Modifications of hiv env, gag, and pol genetic immunization
Patent: WO 0232943-A 165 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)

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Best Local Sim
Matches 2174;
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                                    TGCCCGCCCACAAGGGCATCGCCGCCAACGAGCAGCAGCAAGGGCA
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iive 0; Mismatches 185;
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Modifications of hiv env, gag, and pol-
genetic immunization.
Patent: WO 0232943-A 176 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
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PAT 20-JUN-2002

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AX427933

RESULT 11 AX427933 LOCUS

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                                                                                 Huang,Y. and Nabel,G.J.
Modifications of hiv env, gag, and pol enhance immunogenicity genetic immunization
Patent: WO 0232943-A 171 25-APR-2002,
GOVERNMENT OF THE UNITED STATES (US)
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Pred. No. 3.9e-197;
0; Mismatches 189;
                                                                                                                                                               construct'
Sequence 171 from Patent WO0232943. AX427933
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/organism="synthetic cc/db_xref="taxon:32630"
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artificial sequences.
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TCGTGAACACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCG
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                                 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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Modifications of hiv env, gag, and pol
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Patent: WO 0232943-4 166 25-APR-2002;
GOVERNMEN OF THE UNITED STATES (US)
Location/Qualifiers
1. 9170
//organism="synthetic constru/db_xref="taxon:32630"
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3027 TCGCAACCAGCGCAAGATGTGAAGTGCTTCAACTGCGGCAAGGGGCCACACGCCCC
                                                                            311 TGCAGGTGCGCGG-----CGACAACCCCCGCAGCGAGGCCGGCGCGCAGGGCCAAGGGCA
                                                                                                                                                                                                                                                                                                                                  3261 TTCAGGTTTGGGGAAGAGACAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAA
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                                                        131 GCAACTGCCGCGCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGA
                                                                                                                                     191 TGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCGCGCGAGGACCTGGCCTTCCCCCAGG
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                   CCGAGATCGTGATCTACCA-----GGCCCCCTGTACGTGGGCACCTGGACGTGGACATCG 1252
                              GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 1666
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4101 GCCCCGCCATCTTCCAGTGCAGCATGACCAAGATCCTGGAGCCCTTCCGCAAGCAGAACC 4160
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                  2267 TGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCA
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                                                                              191 TGAAGGACTGCACCGAGGCCAACCTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="plasmid pvR1012x/s containing HIV genes"
2895 c 2719 g 1829 t
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                                                                 TCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTA
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Modifications of hiv env, gag, and pol
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Patent: WO 0232943-A 173 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
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| Qy Db | 539 | AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG : | 598 4172 |
|----------|-------------|---|--------------|
| Qy | 599 | TGACCCAGCTGGGCT TGACCCAGATCGGCT | 658 4232 |
| Qy | 659 | GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA | 718 |
| Qy Db | 719 | TGGACGCCCCAAGGIGAAGCAGTGGCCCCTGACCGAGAGAGAAGATCAAGGCCTGACG (| 778 |
| Qy Db | 779 | CCATCTGCGAGGAGATGGAGAGGAGGCAAGATCACCAAGATCGGCCCGGAGAACCCCT | 838 |
| Qy | 839 | ACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGG : | 898 4472 |
| Oy Db | 899 | ACTICCGCGAGCTGAACAAGCGCACCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCC | 958 4532 |
| Qy Db | 959 4533 | ACCCGCCGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT | 1018 4592 |
| Oy Db | 1019 | TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA | 1078 |
| Qy Dp | 1079 | ACAACGAGACCCCGGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA | 1138 |
| Oy Dp | 1139 | GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC | 1198 |
| Oy Db | 1199 | CCGAGATCGTGATCTACCAGGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG | 1252 |
| oy Db | 1253 | GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCA | 1312 |
| Qy Db | 1313 | CCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCATCGAGCTGCACCC | 1366 4952 |
| Qy | 1367 | CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGCGTGGACCGTGAACG | 1426 5012 |
| Qy | 1427 | ACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCA | 1486 5072 |
| Qy | 1487 | TGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCTGA | 1546 5132 |
| Oy Dp | 1547 | CCGAGGAGCCGAGCTGGAGCTGGCCGAGAACCGCGAGAATCCTGCGCGAGCCCGTGCACGCAC | 1606 5192 |

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PAT 20-JUN-2002
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0232943-A 172 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
1. .978
/organism="synthetic construct"
/db_xref="taxon:32630"
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GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 1666
                                                              5253 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCC
                                                                                                                                                                                                                                                5553 GCGCCGAGACCTTCTACGTGGACGCCCCCCAACCGCGAGACCAAGCTGGGCAAGGCCG
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                                                                                                                                                    1787 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG
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              1727 AGATGCGCACCGCCCACAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG
                                                                                                               GCGCCGAGACCTTCTACGTGGACGGCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
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1546 GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCCGCAACC 1198 1312 1366 4217 4337 1606 1846 4817 4577 4637 1786 4757 GCTACGTGACCGACCGGGCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGGA 2086 TCAGCGTGCCCCTGGACAAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA CCGAGATCGTGATCTACCA-----GGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG GCCAGCACCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGCTGGGGGCTTCACCA AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA ACCCCGCCGCCCTGAAGCAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCAGCATCA ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA CCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGCCCAT-----CGAGCTGCACC CCGACAAGTGGACCGTGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACG TGCGCCAGCTGTGCAAGCTGCTGCGCGCCCAAGGCCCTGACCGAACATCGTGCCCTGA CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG CCGAGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGCCCGTGCACG 1727 AGATGCGCACCGCCCACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGG AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT TCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGGAGGAGCCCATCATCG GCGCCGAGACCTTCTACGTGGACGCCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCG GCGCCGAGACCTTCTACGTGGACGGCGCCGACCGCGAGACCAAGCTGGGCAAGGCCG 3918 1019 1139 1199 4218 4278 (3978 1079 4038 1313 1367 1253 4338 1427 4398 1487 4458 1547 4518 1607 4578 1667 4638 4698 1787 4758 1847 4818 1907 4878 1961 4938 2027 g ò g ŏ q $^{\circ}$ QΣ g δy g ŏ qq δ qq qq g Dp Qγ δ δλ QΥ q ŏ qq ò QQ à qq g q ò ά $^{\circ}$ a ŏ

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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: Wo 0232943-A 170 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
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4998 GCTACGTGACCGACCGCGCCGCCAGAAGGTGGTGCCCCTGACGACACCACCACCACCAGA 5057
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                                  AGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGGCCTGGG
                        AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCG
                                                                                                                  AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG
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Pred. No. 3.9e-197;
0; Mismatches 189; Indels 33;
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//db_xref="taxon:28630"
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Matches 2173; Conservative
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3261 TTCAGGTTTGGGGAAGAGACAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAA 3320
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OM nucleic - nucleic search, using sw model

2003, 10:51:03; Search time 489.804 Seconds (without alignments) 11296.684 Million cell updates/sec February 10, Run on:

US-09-610-313-32 2457 Perfect score: Title:

1 gtcgacgccaccatggccga......gggctagcaccggtgaattc Sednence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2185239 segs, 1125999159 residues Searched:

4370478 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result

Synthetic construc Synthetic construc Synthetic construc HIV FS(-)_ProtMod_ Modified HIV prote Description ABK91616 AAA70481 ABK91622 ABK91617 ABL39960 ABL39959 AAA70479 ABL39961 AAA70480 DB Match Length 2457 2463 2463 2469 2300 2306 9166 2312 9788 1000.0 99.2 98.3 83.0 82.2 81.4 81.3 81.3 Query 2457 2436.2 2415.4 2040 2019.2 2000.8 1998.4 1992.4 Score

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ALIGNMENTS

Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds. Van Rensburg EJ; Engelbrecht S, Synthetic construct PR975YMWM SEQ ID NO:32. Human immunodeficiency virus type C. ВР ABL39961 standard; DNA; 2457 05-JUL-2001; 2001WO-US21241. 05-JUL-2000; 2000US-0610313 Zur Megede J, Barnett SW, (first entry) (CHIR) CHIRON CORP. (UYST-) UNIV STELLENBOSCH. WO200204493-A2 15-MAY-2002 17-JAN-2002 Synthetic. ABL39961; RESULT 1 ABL39961

New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy

Claim 1; Fig 10; 233pp; English.

The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of the present invention.

Seguence 2457 BP; 566 A; 837 C; 754 G; 300 T; 0 other;

Query Match 100.0%; Score 2457; DB 24; Length 2457; Best Local Similarity 100.0%; Pred. No. 1.9e-297; Matches 2457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

- 61 CGCAGCAACTTCAAGGGCCCCAAGGGCTCATCAAGTGCTTCAACTGCGGCAAGGGGC 120

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- Db 61 CGCAGCAACTICAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGGGCC 120
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 - Db 121 CACATCGCCCGCAACAGCCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGAGGAG
 Qy 181 GGCCACCAGATGAAGGACTGCACCGAGGCCAAGCAACAACAACAAGAACTGCAGGCCAAGCTGCAAGAAGGACTGCAGCCCGAGGCCAACTTCTCCGCGAAGAACTGCAGGCC
- 181 GGCCACCAGATGAAGACTGCACCGAGCGCAAGCTTCTTCCGCAGAGCTGGCC

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- Db 481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATCGCGGGCATCGGCGGCTTCATCAAG
 Qy 541 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG

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- Qy 721 GACGGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC 780

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Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds.
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The present invention describes expression cassettes comprising a polypuched comprising indepthed sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Mef (1). (1) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the
                         in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy
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                                                                                                                                                                                                                                                                                                                                     99.2%; Score 2436.2; DB 24; Length 2463; 99.6%; Pred. No. 7.2e-295; 11ve 0; Mismatches 3; Indels 6;
                                                                                                                                                                                                                                                                                                        Sequence 2463 BP; 567 A; 835 C; 759 G; 302 T; 0 other;
                                                                                                                                                                                                                                                                         exemplification of the present invention.
                                                                                      Claim 1; Fig 9; 233pp; English.
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WPI; 2002-154920/20
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            1855 GAGACCIGGIGGACCGACTACIGGCAGGCCACCIGGAICCCGAGIGGGAGITCGIGAAC
                                                                      1861 GAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC
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Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; immunostimulant; gene therapy; gene; ds. Synthetic construct PR975(+) SEQ ID NO:30. BP. ABL39959 standard; DNA; 2469 (first entry) 15-MAY-2002 ABL39959; RESULT 3

Human immunodeficiency virus type C. Synthetic.

WO200204493-A2.

nef;

05-JUL-2001; 2001WO-US21241. 17-JAN-2002

05-JUL-2000; 2000US-0610313

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The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding day Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL30942 to ABL40064 and ABB00204 to ABB00215 represent sequences used in the
                                                                                                                                                    New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy
                                                                             Van Rensburg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention.
                                                                             Engelbrecht
                                                                                                                                                                                                                                Claim 1; Fig 8; 233pp; English.
                                                                           Zur Megede J, Barnett SW,
                  CHIRON CORP.
UNIV STELLENBOSCH
                                                                                                                WPI; 2002-154920/20
                (CHIR ) (UYST-)
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Sequence 2469 BP; 571 A; 833 C; 761 G; 304 T; 0 other;

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180 360 420 480 540 99 480 CGCAGCAACTICAAGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC 120 Gaps GTCGACGCCACCATGGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG 60 CGCAGCAACTTCAAGGGCCCCCAAGCGCATCAAGTGCTTCAACTGCGGCAAGGAGGGC CACATCGCCCGCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCCGCCAAGGAG GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTG GTGCGCCAGTACGACCAGATCCTGATCTGCGGCAAGAAGGCCCATCGGCACGTG 601 CTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGC GGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCC TICCCCCAGGGCAAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACC AGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCAGCGAGGCGCCGGCGCGCGAG GGCGGCCAGATCAAGGAGGCCCTGCACACCGGCGCGCGACGACGACGTGCTGGAGGAG ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATCGGCGGCGATCGGCGGCTTCATCAAG GTGCGCCAGTACGACCAGATCCTGATCTGCGGCAAGAAGGCCCATCGGCACGTG 98.3%; Score 2415.4; DB 24; Length 2469; larity 99.3%; Pred. No. 2.8e-292; Conservative 0; Mismatches 6; Indels 12; 0 12; Indels Best Local Similarity Matches 2451; Conserv Query Match 61 61 21 121 181 241 541 181 241 301 481 301 361 361 121 421 481 541 Qγ Qγ g g οy Db δŏ g QΥ QQ οχ Db ò Db δ Ω δ qq δy a δ

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                              ACCGACAGCCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCGAG
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                                                          ATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAG
                                                                                               ACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCCGAGTGGGAGTTC
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                                                                                                                                                                     Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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Pred, No. 1.3e-245;
0; Mismatches 135;
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C;
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93.6%;
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Walker
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Matches 2153; Conservative
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Selby M, Wal
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                                                                             (CHIR ) CHIRON CORP
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                                           AGAAGATCAAGGCCCTGGTGGAGATCTGCACCGAGATGGAGAAGGAGGGCCAAGATCAGCA
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           TCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCG
                                                                                CCATCATCGGCGCGCGAGACCTTCTACGTGGACGCGCCGCCGAACCGCGAGACCAAGATCG
                                                                                                                       GCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCA
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                                                                                                                                                                        1921 CCAACCAGAAGACGGAGCTGCAGCCATCCACCTGGCCCTGCAGGACAGGGCCTGGAGG
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                                        AGTGGGAGTTCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGC
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                                                                                                                                                          The present sequence is the coding sequence of a synthetic HIV Gag-reverse transcriptase expression cassette, FS(-)_brotWod_RTopt_YM. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of th HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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           AGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGGGGCA 2131
                                                                                                                                            GCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCG 2191
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                                               AGATCGGCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCG
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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                                                              The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ARK91449-ABK91634 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
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                                                                                                                                                                                                                                                                                                                          DB 24; Length 9166;
                                                                                                                                                                                                                                                                                      Sequence 9166 BP; 2227 A; 2662 C; 2513 G; 1764 T; 0 other;
                                                                                                                                                                                                                                                                                                                        81.4%; Score 2000.8; DB 24; Lengt
91.3%; Pred. No. 7.6e-241;
iive 0; Mismatches 182; Indels
                                Disclosure; Page 766-769; 794pp; English.
immunodeficiency virus infection
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| CTGCGAGGAGAAGGAGGGAAGATCACCAAGATCGGCCCCGAGAACCCCTAC | CGGCGGCCTGAAGAAGAAGAGGGTGACCGTGGACGTGGGCGACGCCTATCA CGGCCGCCCGAAGAAGAAGAGGGTGACCGTGGACGTGGGCGACGCCTATCA CGGCCGCGCCTGCAAGAAGAAGAAGACGTGCACCGTGGACGCGACGCCTACACTTCA GCGTGCCCCTGGACGACGACTTCCGCAAGTACACGCCTTCACCATCCCCAGCATCAACA GCGTGCCCCTGGACAAGACTTCCGCAAGTACACCGCCTTCACCATCCCAGCATCAACA ACGAGACCCCCGGCAACGACTTCCGCAAGTACAACGCCTTCACCATCCCCAGCATCAACA ACGAGACCCCCGGCAACGAACTACAACAGTCCCCAGGGCTGGAAGGGCAGCC ACGAGACCCCCGGCAACCAGTACAACAGTCCCCAGGGCTGGAAGGGCAGCC | CGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGG CAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCC CGCCATCTTCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCAACCCC GGCCATCTTCCAGTGCAGCATGACCAAGATCCTGGAGCCCTTCCGCAAGCAA | CATCGTGATCTACCAGTACATGGACCACCTGACGCAGCGACCTGGAGATCGGC GCACCGCGCCCAGAGACTGGCCAACCACCTGCTGCGCTGGGCTTCACCACC IIIIIIIIIIIIIIIIIIIIIIIIIIIII | CCGACAAGAAGCACCCCCTTCCTCCCCCCATCGACCCCCCCCCC | ###################################### | AGGAGGCCGAGCTGGAGGAACCGCGAGATCCTGCGCGAGCCCGTGCAGCCG 111111111111111111111111111111111111 | GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACTGAAGACCGGCAAGTACGCCAAGA | GGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCTCCAGAAGAG |
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HIV-1; AIDS; Gag-reverse transcriptase; vaccine; expression cassette; ss
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1850 CCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG 1909
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           4820 CCTGGGGGGCCTGGTGGACCGAGTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG
                                                    2090 CCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGGCAGCGGCAGCGAGGTGAACATCGTGA
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C;
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99US-0168471.
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Selby M, Walker
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Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -

Claim 7; Fig 75; 391pp; English.

us-09-610-313-32.rng

The present sequence is the coding sequence of a synthetic HIV
dega-reverse transcriptase expression cassette, FS(-)_protMod_RTopt(+).
The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV dega-polypetides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS)

Sequence 2312 BP; 533 A; 750 C; 732 G; 297 T; 0 other;

4; 170 GCGGCAAGGAGGCCACCAGATGAAGGACTGCACCGAGCCCAGGCCAACTTCTTCCGCG 229 AGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCA 289 397 457 420 637 480 697 757 009 817 Gaps 9 AGGACCTGGCCTTCCTGCAGGGCAAGGCCCGCGAGTTCAGCAGCGAGCAGACCCGCGCCA ----AACTTCCCCCAGATCACCCTGTGGCAGC GCCCCTGGTGACCATCAGGATCGGCGGCCAGCTCAAGGAGGCGCTGCTCGACACCGGCG GCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCG CCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCG GCGCCATCGGCGCCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCG GCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCCACCCCCGTGAACATCATCGGCCGCA ACATGCTGACCCAGCTGCACCCTGAACTTCCCCCATCAGCCCCATCGAGACCGTGC AGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCA CCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGG AGAICGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCA CCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGG AGGTGCAGCTGGGCATCCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAAGAGCGTGACCGTGC 2312; 24; DB 21; Length 141; Indels Score 1998.4; DB 23 Pred. No. 1.8e-240; 0; Mismatches 141; CCGGCCCCGAGCGCCAGGGCACCCTG-81.3%; 92.9%; st Local Similarity 92.9 tches 2147; Conservative Query Match Ч 230 61 290 121 181 398 241 458 518 361 541 758 818 344 301 421 181 869 601 199 878 938 721 ŏ qq ŏ q a g Dρ pp οy δ Ω QΥ g Ω α g δ δŽ ΩŸ q óλ Op δ Db Qγ g ò

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1117 1177 1351 1465 TGACCGAGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACA 2125 900 TGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCG CCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGC TGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGG AGCCCTTCCGCGCCCCCCCCGAGATCGTGATCTACCA-----GGCCCCCCTGTACG 1021 AGCCCTTCCGCAAGCAGCACACGCGACATCGTACCAGTACATGGACGTGCTGTACG AGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGGGCCAGCC TCCGCCTGCCCATCCAGAAGGAGCCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCA CCTTCACCATCCCCAGCATCAACAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGC TGGGCAGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACC TGCTGCGCTGGGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGC CCAT-----CGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGA AGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGGAACTGGGCCAGCC AGATCTACGCCGGCATCAAGGTGAAGCAGCTGTGCAAGCTGCTGCGCGGCACCAAGGCCC TGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGACGAGAACCGCGAGA TCCTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGA TCCAGAAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACC TGAAGACCGGCAAGTACGCCAAGATGCGCACCACCACCAACGACGTGAAGCAGCTGA CCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCCAAGACCCCCAAGT CCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCTGGTGAAGCTGTGGTACCAGC TGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGCGCCCCCAACCGCG AGACCAAGATCGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGATCGTGAGCC 841 1058 901 1118 1178 1232 1292 1261 1646 1081 866 1352 1406 1466 1321 1526 1381 1586 1441 1561 1706 1766 1621 1826 1681 1946 1801 2006 1861 2066 1501 1886 1741 d δy q δ q δ g δ g δ qq δ qq ŏλ Q ò g Op Db á ò Qγ g δ g δ qq δŽ Op ŏ δŏ a δ d δ

us-09-610-313-32.rng

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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human
                                                                                                                                                 2100
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1921 TCGCCGACACCACCAACCAGAAGACCGAGCTGCAGCCATCCACCTGGCCTGCAGGACA 1980
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14-NOV-2000; 2000US-252115P.
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            antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Gag, Pol or Nef: Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
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Immunodeficiency syndrome (AIDS) or HIV infection and generating an
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                                                                                                                  Sequence 9788 BP; 2377 A; 2817 C; 2695 G; 1899 T; 0 other;
                                                                                  plasmid DNA sequences of the invention.
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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CTL.
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ACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGAGCCACCAGAAGA
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immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding DNA sequences of the invention. plasmid

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Sequence 9169 BP; 2227 A; 2668 C; 2505 G; 1769 T; 0 other;

9 Gaps 80.5%; Score 1978.4; DB 24; Length 9169; ilarity 91.1%; Pred. No. 4.6e-238; Conservative 0; Mismatches 186; Indels 28; Best Local Similarity Matches 2178; Conservat Query Match

2967 regecedadeceargaceadergeageacaceaceacarcargargeagecegecaacrrca 3026 73 14 TGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTCA à

AGGGCCAGAAGCGCAT---CAAGTGCTTCAACTGCGGCAAGGAGGGCCCACCTGGCCCGCA 3083 AGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCCGCA 133 3027 74 g

ACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGA 193 ACTGCCGCGCCCTGCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGA 3084 134

ò g ò Db δ QQ à g δ g ò g

AGGACTGCACCGAGCGCCAGGCCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCA 3144 194

313 **AGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTGC** AGGCCAGGGAATTTCTTCAGAGCAGACCAGACCAACAGCCCCACCAGAAGAGAGCTTC 3203 254

364 AGGTGCGCGG-----CGACACCCCCGCAGCGAGGCCGGCGCGCGAGCGCCAGGGCA---314

421 AGGTTTGGGGAAGAGACAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGGAACTG 3263

3382 ---CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCTGG 365

TGAGCCTGCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGCTTCATCAAGG TGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGC 542 482 ò Op ò

3503 g

3622 TGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCA 3563 602 Óγ qq

781 ACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCA 722 Ω g

CCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG

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CCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG

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841 TCTGCGAGGAGATGGAGGAGGAGGCCAAGATCACCAAGATCGGCCCCGAGAACCCCTACA 3683 782 ŏ

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ACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT 842 3803 ò

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1369 1315 GCCAGCTGTGCAAGCTGCTGCGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCG 1549 1141 4102 4162 1255 4282 1021 1081 1201 ACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACGACA ACAAGTGGACCGTGCAGCCCATCGTGCTGCCCGAGAAGGACAGCTGGACCGTGAACGACA 902 TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACC 3863 TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACC 962 CCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTCA GCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACA ACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCC 4043 ACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCC CCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCG AGATCGTGATCTACCA-----GGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCC AGCACCGGGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACCC CCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCAT-----CGAGCTGCACCCCG TCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGC 1022 (1142 1316 1370 4343 1430 1490 4463 1082 1202 1256 q g g g δy g δ qq Ω g ò 엄 QΥ g Qγ 셤 ò g Qγ δ QΥ

CCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGCT 2029 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGA 1729 TGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG 4643 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGCGAAGTACGCCCGCA TGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGCCGTGCAGAAGATCGCCA TGAAGGGCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA CCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG TGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG 4823 1670 1730 4703 1790 1850 1910 4883

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TGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACAGT 4583 TGTACTACGACCCAGCAAGAACTGATCGCCGAGAATCCAGAAGCAGGGCCAGGT

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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gay. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CTL.
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                                                                                    CCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCC
                                                     ACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCACCAGAAGA
                                                                                                                    2090 CCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCGGCGGGGGGAGGTGAACATCGTGA
                                                                                                                                                                                      TGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                            2330 GCAAGGIGCIGIICCIGGACGGCAICGAIGGCGGCAICGIGAICIACCAGIA 2381
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28-MAR-2001; 2001US-279257P.
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immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
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                                                                                                         Sequence 9194 BP; 2232 A; 2672 C; 2523 G; 1767 T; 0 other;
                                                                                                                                                                      Indels
                                                                                                                                      80.4%; Score 1975; DB 24;
90.9%; Pred. No. 1.2e-237;
iive 0; Mismatches 190;
                                                                            DNA sequences of the invention
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Matches 2177;
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                ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA
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                                                                        3986 TCAGGGTGCCCCTGGACAAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA
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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV BIV, cay, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired
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TGCCCGCCCACAAGGGCATCGCCGCCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCA
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                                                                                                                                            2147 TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCG
                                                                                                                                                                                                  AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified human immunodeficiency virus Env, Gag, Pol of Nef its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified HIV protein-encoding plasmid DNA #163.
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14-NOV-2000, 2000US-252115P.
28-MAR-2001, 2001US-279257P.
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immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.

SSSSSSXS

Seguence 9194 BP; 2232 A; 2671 C; 2524 G; 1767 T; 0 other;

9 Gaps DB 24; Length 9194; Indels 80.3%; Score 1973.4; DB 24 llarity 90.9%; Pred. No. 1.9e-237; Conservative 0; Mismatches 191; Similarity 2176; Match Local Matches Query

70 δ Dp

TCCGCAACCAGCGCAAGATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACACCGCCC 3086 130 TCAAGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 3027 QΥ g

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598 AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCCGCTTCATCA 3446 AGATGAACCTGCCCGGCCGCTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCA QC QΥ Óγ

3565 3506 AGGIGGGCCAGTACGACCAGAICCIGATCGAGAICIGCGGCCACAAGGCCAICGGCACCG AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCG qq

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3685 718 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCCA 629 g Óγ

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AGATCTGCACCGAGAGAGAGAGAGGAGAAGATCAGCAAGATCGCCCCGGAGAACCCT CCATCTGCGAGGAGATGGAGAAGGAGGCCAAGATCACCAAGATCGGCCCCGAGAACCCCT pp

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868 ACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG 3806

GCGCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCG 2026

1961

1546 1078 4105 GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC CCGAGATCGTGATCTACCA-----GCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCCAGGGCTGGAAGGGCA GCCAGCACCGCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGCTGGGGGCTTCACCA CCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGCCCAT-----CGAGCTGCACC TGCGCCAGCTGTGCAAGCTGCTGCGCGCGCGCCCAAGGCCCTGACCGACATCGTGCCCCTGA ACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC ACCCCGCCGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCTACT ACCCCCCCCCCCCTGAAGCAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 3866 3926 1019 3986 1079 4046 1139 4106 1199 4166 1253 4226 1313 4286 1367 4346 1427 4406 1487 668 959 qq g g d Qγ q δ q Ω qq δy g Ω δy g δλ d δ ŏ δ

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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gay. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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TGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGGATCGACAAGCTGGTGAGCAAGGGCA
                                                      GCTACGTGACCGGCCGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGAACCAGA
                                                                                             AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGCAGCGAGGTGAACATCG
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(CHAD/) CHADRABARTI B K.
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immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
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                                                                                                                                                        80.3%; Score 1973.4; DB 24; Length 12411; 90.9%; Pred. No. 1.9e-237;
                                                                                                                        Sequence 12411 BP; 2938 A; 3733 C; 3476 G; 2264 T; 0 other;
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                                                                                      plasmid DNA sequences of the invention.
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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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| immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HI Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subse compositions are useful for treating or preventing HIV infections o AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-en plasmid DNA sequences of the invention. Sequence 9785 BP, 2360 A, 2843 C, 2731 G, 1851 T; 0 other; | Match 80.2%; Score 1970; DB 24; Length 9785; Local Similarity 90.9%; Pred. No. 5.1e-237; es 2174; Conservative 0; Mismatches 185; Indels 33; Ga | 14 TGGCCGAGGCCATGAGCCAGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTCA | 74 AGGGCCCAAGGGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCGGCA | 34 ACTGCCGCGCCCCCGCAAGAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGA | 94 AGGACTGCACCGAGCGCCAGCTACTTCCGCGAGGACCTGGCCTTCCCCAGGGCA | 54 AGGCCCCCGCGAGTTCCCCAGCCAGCAGAACCGCCCAACAGCCCCACCAGCGCGCGAGCTGC | 14 AGGTGCGCGGCGACAACCCCGCAGCGAGGCCGGGCGCGAGGCCAGGGCA | 65CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGG . | 22 GCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGGAGA | 82 TGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGG 1 1 1 1 1 1 1 1 1 | 42 IGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGACCCATCGGCACCGTGC | 02 TGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCG | 62 CCCTGAACTICCCCATCAGCCCCATGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGG | ACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC | B2 TCTGCGGGGGGGTGGAGGGGGGAGGTCGCCGAGGGCCCCGGGAACCCCTACA | 42 ACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT |
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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gay. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic I lymphocyte; CIL.
DNA and
                                                                                                    TGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGC
                                      ACGTGACCGACCGGCCGGCAGAAGATCGTGAGCCTGACCGAGGACCACCAGCAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified human immunodeficiency virus Env, Gag, Pol of Nefits encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
                                                                                                                                                                                                                                                                                                      2330 GCAAGGTGCTGTTCCTGGACGGCATCGATGGCGCCATCGTGATCTACCAGTA 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified HIV protein-encoding plasmid DNA #171.
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Gag, Pol or Nef: Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
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                                                                                                                                  80.0%; Score 1966.6; DB 24; Length 9167; llarity 90.7%; Pred. No. 1.4e-236; Conservative 0; Mismatches 189; Indels 33;
                                                                                                     Sequence 9167 BP; 2225 A; 2668 C; 2517 G; 1757 T; 0 other;
                                                                           plasmid DNA sequences of the invention
                                                                                                                                                  Similarity
                                                                                                                                                               Matches 2173;
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                  3858 ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGGATTCCCCC
                                      959 ACCCCGCCGCCTGAAGAAGAAGAAGAGCGTGACCGTGCACGTGGACGTGGCCGACGTACT
                                                1079 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA
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The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular
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4938 GCGCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGCTGGGCAAAGGCCG
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                                                                                              5298 TCCGCAAGGTGCTGCTGGACGGCATCGACAAGGCCCAGGAGGAGCACGAAA 5352
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immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
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BM321022 rockefell
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    Anote="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Malze Mapping Project"
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                                         ACCCCGAGATCGTGATCTACCAGGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCC
                                                                               945 AGGTCATGAACGGCAAGCCCGAGTACACGGACCACCTGACCCACAAGCTGAAGCACACCACC
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/organism="Mastigamoeba balamuthi"
/organism="ATCC 30984"
/db_xref="taxon:10860"
/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
                  951 bp mRNA linear EST 03-JAN-200 cockefeller.0.1211 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to adenosylhomocysteinase (EC BM321451
                                                                                                                                                                                                                                                                                                                                            The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Scl. U.S.A. 99 (3), 1414-1419 (2002) 21819461
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 951)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1842 GAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGGAGTG 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1902 GGAGTTCGTGAACACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCAT 1961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1962 CATCGGCGCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGATCGGCAA 2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2022 GGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAA 2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1082 CCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCGGCGAGGTGAA 2141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2142 CATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGGGA 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 GGCCAAGATCCGCTGGTGCTCGTGCAACATCTTCTCGACGCAGGACCACGCGGCCGCCGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 CATCGCGCAGGCCGCGTCTCGGTCTTCGCCTGGAAGGGCGAGAACCTCCAGGAGTACTG 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 CGACGGCGTGACGCGACTCTGATGATCCACAAGGGGTTCGCGGGCCGAGGACAACCCCAA 458
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
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0; Mismatches 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmuller@rockvax.rockefeller.edu
Insert Length: 951 Std Error: 0.00
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46.0%; Pred. No. 0.0
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                                                                                                                                                                                                    Mastigamoeba balamuthi.
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Matches 323; Conservative
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RESULT 2
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EST 03-JAN-2002
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/note="syn: Phreatamoeba balamuthi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM320864 1132 bp mRNA linear EST 03-JAN-200 rockefeller.0.46 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostellum, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                           2202 GAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAG 2261
                                                                                                                                                                                                                               2322 GGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTA 2381
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Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
639 GTTCCCGGCCGTCAACGTCAACGAC---TCTNTCACCAAGAGCAAGTTCGACAACATCTA 695
                                                                                                                                                                                                                                                                          816 CGCCAGGCTGCCGCGTCATCGTGACGGAGATCGACCCCATCTGCGCGCTGCAGGCGTC 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 CGCGCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGAC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 CGCCGCGAGGGCAAGACGGACTACCGCGCGCGCCANCTGGTGATCCAGGACAAGAACAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 IGCACCGAGCGCCAAGTTCTTCCGCGAGGACCTGGCCTTCCCCCGAGGGCAAGGCC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 TACAACAGCCCCAAGTACGCTTCGTC----GTCCGCTTCACCAACAGGGACATCGTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 TGCCAGATCGCCTACGCCAAGATCGACGGCGACCACATCCTCGCCGCCGCCTACTCGCAC 252
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                                                                                                                                                                696 CGGCTGCCGCCACTCGCTCATCGACGCATCAAGCGCGGCACCGACGTGATGCTCGGCGG
                                                                                                                                        2262 CTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAA
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Pred. No. 0.00085;
0; Mismatches 444; Indels 9;
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba
1 (bases 1 to 1132)
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                                                                                                                                                                                                                                                                                                                        2382 CATGGACCTGTACGTGGGCAGCGGCCCTAGGATCGA 2423
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/organism="Mastigamoeba balamuthi"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Rockefeller University 1230 York Avenue, New York, NY 10021, U Email: mmuller@rockvax.rockefeller.edu Insert Length: 1132 Std Error: 0.00
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/db_xref="taxon:108607"
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Best Local Similarity 45.3
Matches 375; Conservative
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/clone_lib="Mastigamoeba balamuthi lambda 2AP II Library"
/note="syn: Phreatamoeba balamuthi"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 CAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCGGCGAGCTGCAGGTGCGCGGCGACAA 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 CAACGGCGAGGACTACAACGTCGAGGAGCTCGACGGGCCCCGCCGTTCAAGGCCC-- 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 GGGCATGTGCGACGGCGTCAACGTCCCCCACAGGCGAGACCCGCTTCGTCGGCTTCAA
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                                                                                                                                                                                                                          3.2%; Score 79.6; DB 13; Length : ilarity 45.1%; Pred. No. 0.0011; Conservative 0; Mismatches 506; Indels
                                                                                                                                            4 others
/organism="Mastigamoeba balamuthi"
/strain="ATCC 30984"
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Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIGAACAICAICGGCCGCAACAIGCIGACCCAGCIGGGCIGCACCCIGAACIICCCCAIC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679 AGCCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCCAAGGTGAAG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 GGCGGCCACGTCGCCGCGTACATGAAGCTCCTCAAGGAGCAGGACGCCGCCGCCCTTCGAC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 CGCCAGTICTCGCGCTACGCCAAGGAGGGTGTCACCGCCGACATGCTCGAGAAGATCTAC 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           730 ACCGAGGCCCACAAGCAGATCCGCGCCGACCCTTCGTCCCCAAGCGCGCCTCGAAG 789
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                             253 GAGCTCACCCGCTTCGGCGTCAAGCTCGGCCTGACCAACTACGCCGCCGCCTACGCGACT 312
                                                                                                                                               313 GGCCTGCTGCTGCCGCCGCGTGTGCTGAAGAAGCTCAACCTCGACTCCAAGTACGAGGGT 372
                                                                                                                                                                                                                                         CAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                             433 TTCAAGGCCCTGCTCGACGTCGGCCTGGTCCGCACCTCGACTGGCGCCCGCGTGTTCGCC
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1165)
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Insert Length: 1165 Std Error: 0.00
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The Rockefeller University
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/strain="ATCC 30984"
/db_xref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi"
/clone_siph="yn: Phreatamoeba balamuthi"
298 c 254 g 124 t 6 others
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                                                                                                                                                                                                                                                                                             Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 867)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 CCGCACAAGATGCGCGAGTGCCTGCCGGTCATCCTGCTGCGCAACAGGTTGAAGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 GCGCTGACCCGCCGTGAGGTCACCTCGATCGTGATGCAGCGCCTGATCAAGATCGACGGC 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 CAGCGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 GCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCC 297
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930 CGGTGCCCTGTACACCGCCATCTCCCGCTGCGGCGTTGCGTTGCGTGGCTTGCGG 979
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 867 Std Error: 0.00
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Mastigamoeba balamuthi
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BM321022 1550 bp mRNA linear EST 03-JAN-2002 rockefeller.0.1192 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to adenosylhomocysteinase (EC
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/organism="Mastigamoeba balamuthi"
/strain="ATCC 30984"
/db_xref="taxon:108607"
/clone_ilb="wastigamoeba balamuthi lambda 2AP II Library"
/note="syn: Phreatamoeba balamuthi"
s 528 c 495 g 226 t 19 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1809 GGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGAC 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Pelobionida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1550)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
                                                                                                                                                                                                                                       654
                                                                                                                                                                                                                                                                     671 GGCCACCAGTTCGCGACGCGCTGACCAACGTCATCGGTGATCGGCAAGGCACCAAGTC 730
                                                                                                                                                                                                                                                                                                                                                                                                            731 CTCGTCACGCTGCCCGCCGCCAAGGGCATCAAGAAGTCGATCATCGAGGAGTTCCAGGCG 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 CGCCTGGAAGGCCGAGAACCTCCAGGAGTACTGGGAGTGCACCTGGAAGGCCCTGTGCTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
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475 GAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGGACGGCGGCATCGGCGGCTTC
                                                                                                                                                                                                                                                                                                                                                   655 GGCTGCACCCTGAACTTCCCCCATCAGCCCCATCGAGACCGTGCCGTGAAGCTGAAGCCC
                                                                                                                  535 ATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGC
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45.6%; Pred. No. 0.0034;
tive 0; Mismatches 364; Indels 3;
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
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Insert Length: 1550 Std Error: 0.00
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BM321022
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebyre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
Contact: Charles Hauser
DCMB Box 91000
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//note="Vector: pBluescript II SK-; Site_l: ECORI; Site_2: xhoIf Stress condition II library, constructed by John
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                  2289 CGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGA 2348
                                                                                                                                                                            305 GCACAAGATCCTCCCGAGATCCGCGGTGTCAGCGAGGAGACGACGACGACTGGCGTGATGAG 364
                                                                                                                                                                                                                                                                                                                                  425 TG---TCACCAAGACAAGTTTGACAACATCTACGGCTGCCGCCACTCGTTCACGACG 481
                                    185 CCACAAGGGGTTCGCGGCCGAGGACAACCCCAAGCTGCTGGAGGACGACGACGGGCCTCGA 244
                                                                                                              245 GGAGGTCGCCTGCCTCAACAACGTGCTCAAGGTCCAGAAGGAGCAGCCCGGCTTCTG 304
                                                                                                                                                                                                                                                                365 GCTGTACCAGCTGCACGCGACGCAAGCTGCTGTTCCCGGCCGTCAACGTCAACGACTC 424
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1929 GAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGA
                                                                                                                                                    2049 GCAGAAGATCGTGAGCCTGACCGAGACCACCAACCAGAAGACGGAGGTGCAGGCCATCCA
                                                                                                                                                                                                                              2349 CGGCATCGATGGCGGCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGG
                                                                        482 CATCAAGCGCGGCACCGACGTGATGCTCGGCGGCAAGGTCGCCGTCGTCGCGGGCTACGG
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/db_xref="taxon:3055"
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Davies and Jeffrey McDermott, combines CDNAs from Cc-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + H202 (1, 12, 5, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda SAP II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806.
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

1 (bases 1 to 862)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%; Score 75; DB 13; Length 545; 46.7%; Pred. No. 0.0059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.0059;
0; Mismatches 270; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1664 ACCAGIGGACCIACCAGAICIACCAGG 1690
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Matches 237; Conservative
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/strain="ATCC 30984"

Abz.xref="taxon:108607"

/clone_lib="taxon:atomooba balamuthi lambda ZAP II Library"

/note="syn: Phreatemooba balamuthi"
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The analysis of 100 genes supports the grouping of three highly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 GGAGTGCACCTNGAAGGCCCTGTGCTTCGGCCCCTACCAGGGACCTCAGANCATCGTCGA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 CGACGCCGTGACCCGACTCTAATGATCCACAAGGGGTTCGCGGCCGAGGACAACCCCAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 deccaagarccecrecrecrescacarcrrcresacecacecacecacececec 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 CATCGCCCAGGCCGGAGTCTCGGTCTTCGCCTGGAAGGCCGAGAACCTCCAGGAGTACTG 339
                     divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
21819461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2022 GGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700 CTGCCGCCACTCGCTCATCGACGGCATCAAGCGCGCACCGACGTGATGCTCGGCGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2259 GAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 GTTCCCGGCCGTCAACGTCAACGACTCTGTCACCAAGAGCAAGTTTGACAACATCTACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                             7 others
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                                                                                                        Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mnuller@rockvax.rockefeller.edu
Insert Length: 862 Std Error: 0.00
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                                                                                        Contact: Muller Miklos
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820 CCAGGGCTGCCGC 832
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es 283; Conserv
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RESULT 9 BM321393

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BM321393 853 bp mRNA linear EST 03-JAN-2002 rockefeller.0.1222 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA
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/clone_lib="Mastigamoeba balamuthi lambda 2AP II Library"
/note="syn: Phreatamoeba balamuthi"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 CTGCTCGACGTCGGCCTGGTCCGACCGGCGCCCGCGTGTTCGCCGCCTCAAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 CTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGGC 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 TCGCGCTACGCCAAGGAGGGTGTCACCGCCGACATGCTCGAGAAGATCTACACCGAGGCC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    808 AAGATCACCAAGATCGGCCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAG 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 CTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 CTGGCCCGCCGTGTGCTGAAGAAGCTCAACCTCGACTACGAGTACGAGGGTGTCAAGAAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 AAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 AACGGCGACAAGAAGGAGCTCAACGCCGCGGTCCTCCGCAAGTACATCTTCGGCGGCCAC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 GTCGCCGCGTACATGAAGCTCCTCAAGGAGCAGGACGCCGCCGCCCTTCGACCGCCAGTTC 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          868 AAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAG 927
                                                                                                                                                                                                                                                                                                                                                                              divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
21819461
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                                                                                                                                                                                                                           Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 833)
Bapteste, E., Brinkann, H., Lee, J.A., Moore, D.V., Sensen
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller
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/strain="ATCC 30984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Biochemical Parasitology
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                                                                                                                                                                                                                                                                                              BM587428 566 bp mRNA linear EST 25-FEB-2002 17000687321202 A.Gam.ad.cDNA.bloodl Anopheles gambiae cDNA clone 19600449696110 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celera Anophales gambiae EST project Unpublished (2002) Contact: Holt R.A. Celera Genomics 45 w. Gude Dr., Rockville, MD 20850, USA Tel: 2404533151 Rax: 2404533151 Rax: 2404533151 Rax: MJ Reverse Golumn: 08 Seq primer: MJ Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)" a 202 c 165 g 139 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004 CGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGATCGTGAG 2063
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596 GAGGGCGCCAAGCCCAAGCACTGGGGCAAGCGCAGGCTGACGTACCACGAGGGCAAGAAC 655
                                                                                      656 CGCGTCGCCCAGAAGAAGGTCCGCCTGGGCTACCCCGACGCCCCCAAGAGCCCAGTAAATT 715
                                            928 GACTICTGGGAGGTGCAGCTGGGCATCCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGC 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 GTTCGAGATCGACGCCAACGGCATCCTGCAGGTGTCGGCCGAGGACAAGGGCACGGGCAA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Anopheles gambiae"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
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-cone="19600449966110"
/clone=11b="A.Gam.ad.cDNA.blood1"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.014;
0; Mismatches 217;
                                                                                                                                  988 GIGACCGIGCIGGACGIGGGCGACGCCIACTICAGCG 1024
                                                                                                                                                            716 CCCGGTGCCCTGTACACNGCCATCTCCCGCTGCGGCG 752
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Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatorphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum,
Triticeae; H
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HVCDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="5-45 DAP Spike"
/lab_host="5-45 DAP Spike"
/lab_host="80LR"
/note="Vector: lambda2AP; Site_1: EcoR1; Site_2: Xho1;
Plants were grown in the greenhouse at the University of
Callifornia, Riverside (Fenton, 53 Close, TJ Close). Whole
Spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pbluescript SK(-) cDNA phagemids
(Choi)in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE601575 640 bp mRNA linear EST 22-OCT-2001
HVSWEh0098K08f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0098K08f,
                                                                                                                                                                               2184 CCAGCCCGACAAGAGCGAGAGCGAGGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAA 2243
302 GGCCGCAACGACGACGAGCTACGCGTACACCTGAAGAACCAGCTCGAAGGA 243
                                                                                                                                                                                                                                                                                                242 CAAGCTGGGGGGGGGGGTGTCCGACGACGACGACGAGATGGAGGAGGAGGCGATCGACGA 183
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/clone="HVSMEh0098K08f"
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Seq primer: AATTAACCCTCACTAAAGGG
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Location/Qualifiers
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1 (bases 1 to 500)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ransay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
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ic, EBro03
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                                                         sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ. Wing R. Kleinhoffs A. Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpags/Dgn/31/cover.html)" 230 c 177 g 97 t lothers
The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
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Hordeum vulgare cDNA clone EBro03_SQ004_B09 5', mRNA sequence.
                                        above. For more details on library preparation and
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Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
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                                                                                                                                                                                                                                                                      Length 640;
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                                                                                                                                                                                                                                                                    Score 72.2; DB 10;
Pred. No. 0.017;
0; Mismatches 229;
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BM372120.2 GI:21948499
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                                                                                                                                                                                                                                                                                        Best_Local Similarity 47.79
Matches 209; Conservative
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Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotland, UK

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/note="Vector: pSPORT1; Site_1: Sal 1; Site_2: Not 1; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old waterlogged barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Optic, EBem08
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                                                                                                                                                                                                                                                                                                                                                                               /cultivar="Optic" /db_xref="taxon:4513" /clone="EBro03_SQ004_B09" /clone="EBro03_SQ004_B09" /clone=lib="root, 3 week, waterlogged, cv Optic, EBro03" /tissue_type="root" /dev_stage="3 week" /dev_stage="3 wee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 GGAGGAGGTGACGGTGAAGGTGTCGGCCAAGATGATCTCGGTGACGGGCCCGCGGGCAC 91
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Pred. No. 0.021;
0; Mismatches 229; Indels
                                                                                                                                                                     or
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 seq primer: M13 reverse.
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                                                                                                                                                                                                                                                                                                                                                     /organism="Hordeum vulgare"
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Location/Qualifiers
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Best Local Similarity 47.77
Matches 209; Conservative
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AJ471121 $
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                                       Cardle, L.,
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                              Hedley, P., Liu, H., Caldwell, D., Mccallum, N., Mudie, S., Cardle, Ransay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Ransay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Dupublished (2001)

Don Jan 10, 2002 this sequence version replaced gi:18111970.

Contact: Waugh R, Marshall DF Genome Dynamics/Computational Biology
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: Ml3 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 849 CGTGTTCGCCATCAAGAAGAAGACAACAACAAGTGGCGCAAGCTGGTGGACTTCCGCGA 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                     /organism="Hordeum vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 CTCCCACGTCCAGAACCTCATCACCGGCGTCACAAGGGCTTCCGCTACAAGATGCGCTT
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1. .538
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205 c 149 g
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Triticeae; Hordeum.
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JOURNAL
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 540)
540 bp mRNA linear EST 24-MAY-2002 S00008 Hordeum vulgare cDNA clone S000080191A10F1, mRNA
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                                                                                                                                                                                                                                                                                                                                                             Saren A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
Barley EST's
Unpublished (2002)
Contact: Schulman AH
Institute of Biotechnology
University of Helsinki
P.O. Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 GCICAAGGIGGACGCCIGGITCGGCACCCGCCGCACCATGGCCGCCATCCGCACCGCCAT 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515
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0; Mismatches 229; Indels
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BQ464692 566 bp mRNA linear EST 30-MAY-2002
HF02P20r HF Hordeum vulgare cDNA clone HF02P20 5-PRIME, mRNA
                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
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flowering)"
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                                                                                                                                                                                       Triticeae; Hordeum.

I (bases 1 to 566)

Radchuk, V. Zanag, H. Weschke, W., Potokina, E. and Wobus, U. Barley ESTs from developing seeds

Unpublished (2002)

Contact: Stein Nils

Molecular Markers Group, Department Genbank

Tostitute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, 06466, Gatersleben, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9%; Score 71.6; DB 14; Length 566; 47.7%; Pred. No. 0:021;
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                                                                                                                                                                                                                                                                                                                                                                                                      Email: stein@ipk-gatersleben.de
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                                                                                                               Hordeum vulgare.
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                                      sequence.
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QY 1209 GATCTACCAGGCCCCCT 1226

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Search completed: February 10, 2003, 20:43:52 Job time : 3389.75 secs

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February 10, 2003, 12:14:58; search time 79.8051 Seconds (without alignments) 9441.811 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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2457
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description | Sequence 7, Appli Sequence 11, Appl Sequence 11, Appl Sequence 13, Appli Sequence 15, Appli Sequence 15, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 17, Appli |
|---------------------|---|
| SUMMARIES | US-09-117-217-7 US-09-117-217-7 US-09-117-217-11 US-09-117-217-11 US-08-118-848A-9 US-08-118-848A-9 US-08-188-553-5 US-08-988-5518-1 US-08-988-5518-1 US-08-98-572-15 US-08-98-572-15 US-08-98-518-1 US-08-98-312-13 US-08-98-312-13 US-08-944-449-7 US-09-50-33-32-7 US-08-944-449-7 US-08-944-449-7 US-08-944-449-7 US-08-620-958A-3 US-08-621-958A-3 US-08-620-958A-3 |
| DB | |
| Length | 2601 2601 2601 2601 7399 9709 9709 9709 9737 9737 9738 8933 8933 8933 8933 893 |
| % Query Match | 44444444444444444444444444444444444444 |
| Score | 00000000000000000000000000000000000000 |
| Result No. | |

| Sequence 19, Appl | Sequence 21, Appl | Sequence 800, App | Sequence 800, App | | Sequence 16, Appl | 1, 4 | 1, | 1, | Sequence 56, Appl | Sequence 56, Appl | | Sequence 56, App. | Sequence 1, Appli | Sequence 18, App] | 14, | Sequence 14, App] | Sequence 14, Appl |
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| US-07-743-357-19 | US-07-743-357-21 | US-08-388-353-800 | US-08-488-551B-800 | US-07-743-357-20 | US-07-743-357-16 | US-08-876-546A-1 | US-09-412-252-1 | US-09-079-675-1 | US-08-470-202-56 | US-08-471-770-56 | US-08-468-059-56 | US-09-109-916-56 | PCT-US93-06748-1 | US-09-158-695-18 | US-08-659-251-14 | US-09-256-490-14 | PCT-US96-11445-14 |
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| 3033 | 4113 | 9207 | 9207 | 3856 | 2739 | 2348 | 2348 | 2348 | 9793 | 9793 | 9793 | 9793 | 1680 | 1256 | 3168 | 3168 | 3168 |
| 40.7 | 40.7 | 40.5 | 40.5 | 36.8 | 36.6 | 33.3 | 33,3 | 33.3 | 32.8 | 32.8 | 32.8 | 32.8 | 32.5 | 23.6 | 21.5 | 21.5 | 21.5 |
| 8.666 | 8.666 | 994 | 994 | 904.2 | 8.868 | 818.4 | 818.4 | 818.4 | 805.8 | 802.8 | 805.8 | 805.8 | 798.2 | ٠. | 527.8 | 527.8 | 527.8 |
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| 15-09-117-217-7 | |
| Sequence 7, Application US/09117217 | |
| Patent No. 6221578 | |
| GENERAL INFORMATION: | |
| APPLICANT: de BETHUNE, marie-Pierre | |
| APPLICANT: HERTOGS, Kurt | |
| APPLICANT: PAUWELS, Rudi | |
| TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE | ARE |
| TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY | ¥. |
| | |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*

Database :

ALIGNMENTS

9 Length 2601; TITLE OF INVENTION: HIV POSTITIVE BASED ON TITLE OF INVENTION: HIV POSTITIVE BASED ON TITLE OF INVENTION: OF HUMAN HIV STRAINS; FILE REFERENCE: 1377-125P; CURRENT FILING DATE: 1998-07-24; NUMBER OF SEQ ID NOS: 15; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 250 ID NOS: 15 LENGTH: 2601 ; LOCATION: (1)..(492) ; OTHER INFORMATION: gag Polyprotein US-09-117-217-7 ORGANISM: HIV-HXB2 NAME/KEY: CDS TYPE: DNA FEATURE:

131 GCAACTGCCGCCCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGA 190 71 TCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130 191 TGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGG 250 251 GCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGGGAGC 310 Gaps 28; 44.0%; Score 1081.6; DB 4; Length 67.9%; Pred. No. 4e-169; Live 0; Mismatches 734; Indels Query Match
Best Local Similarity 67.9
Matches 1610; Conservative Q Óλ q g g ò Qγ Q_{Y} δλ g

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GCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCTGCGGGGCTTCACCA 1312
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Sequence 9, Application US/09117217 Patent No. 6221578

; Sequence 9, Applicat; Patent No. 6221578; GENERAL INFORMATION:

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        APPLICANT: HERTOGS, Kurt
APPLICANT: HERTOGS, Kurt
APPLICANT: PADWELS, Rud;
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: HIV POSITITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT APPLICATION NUMBER: US/09/117,217
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO S: 15
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                                                                                                                                                                                                                           44.0%; Score 1081.6; 67.9%; Pred. No. 4e-16
APPLICANT: de BETHUNE, Marie-Pierre
                                                                                                                                                                                  LOCATION: (334)..(489)
OTHER INFORMATION: gag P6 (52 AA)
                                                                                                                                                                                                                                                Matches 1610; Conservative
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                 ORGANISM: HIV-HXB2
                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (33
                                                                                                                             LENGTH: 2601
                                                                                                                                                                                                       US-09-117-217-9
                                                                                                                                         TYPE: DNA
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TGGACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAGATCAAGGCCCTGACCG 778
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                                                                                              ACAACACCCCCGTGTTCGCCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG
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APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: HERTOGS, Kurt
APPLICANT: HERTOGS, Kurt
APPLICANT: PAUWELS, Rudi
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: OF HUMAN HIV STRAINS
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
LENGTH: 2601
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                                                                                                      1936 AAACATGGGAAACATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCCTGAGTGGGAGT 1995
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                                                                                                                                                                        1996 TTGTTAATACCCCTCCCTTAGTGAAATTATGGTACCAGTTAGAGAAACCCCTTAGTAG
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                                                                                                                                                                                                                                                        2056 GAGCAGAAACCTTCTAIGTAGAIGGGCAGCTAACAGGGAGACTAAATTAGGAAAAAGCAG
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                                                                                                                                              GCGCCGAGACCTTCTACGTGGACGCGCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
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                                                              AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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Pred. No. 4e-169;
0; Mismatches 734; Indels
2327 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2358
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Best Local Similarity 67.9%;
Matches 1610; Conservative
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LOCATION: (453)
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US-09-117-217-11
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APPLICANT: de BETHUNE, Ma
APPLICANT: HERTOGS, Kurt
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FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILE DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                           2356 TACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAA 2415
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2296 AGTTAGTCAATCAATAATAATAGAGCAGTTAATAAAAAAGGAAAAGGTCTATCTGGCATGGG
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; OTHER INFORMATION: Reverse Transcriptase
US-09-117-217-13
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US-09-117-217-13
Sequence 13, Application US/09117217
Patent No. 6221578
GENERAL INFORMATION:
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APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: GEORGE G., CHANG-UIE, CHEN, BANJERJEA, AKHIL
TILLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77
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43.8%; Score 1075.2; DB 2
Best Local Similarity 67.7%; Pred. No. 4.9e-168;
Matches 1606; Conservative 0; Mismatches 738;
            MEDIUM TYPE: Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,848A
FILLING DATE: 07-APR-1995
                                                                                                  CLASSIFICATION: 526
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936,849
FILING DATE: 28-AUG-1992
CLASSIFICATION: 5.56
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                REGISTRATION NUMBER: 36,459
REPERBUCK/DOCKET NUMBER: 20,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 7399 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                     212-751-6849
READABLE FORM
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US-08-418-848A-9
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599 TGCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT
                                                       2437 TATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTGGCT
                                                                                                                     659 GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
                                                                                                                                                                                                                                       719 TGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG
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                                                                                  3577 GAATGAAGGCTGCCCACACTAATGATGTGAAACAATTAACAGGGGCAGTACAAAAAATAG 3636
                                                                                                                     CCATGGAGAGCATCGTGATCTGGGGCCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1846
                                                                                                                                                   3637 CCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAATTACCCATACAAAAGG 3696
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: MORDERFECT (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Describers, Ronald C.
TITLE OF INVENTION: PRIMATE LENTIVIRUS VACCINES
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2358
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Patent No. 5851813
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STATE: Massac
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                                                                                                                                                                                                                                                                                                                                                                       Length 9709;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
43.8%; Score 1075.2; DB 2;
Best Local Similarity 67.7%; Pred. No. 5.1e-168;
Matches 1606; Conservative 0; Mismatches 738; 1
                                                                                                                       5851813 29,066
                                                                                                                     Reg. No. 5851813
FR: 00246/079002
                                                APPLICATION NUMBER: 07/551,945
FILING DATE: July 12, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                   NAME: Freeman, John W.
REGISTRATION NUMBER: Reg. NO.
REFERENCE/DOCKET NUMBER: 0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: 07/72:
FILING DATE: 011y 9, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/55:
                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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US-08-188-583-5
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TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2358
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6010895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deacon, Nicholas J.
Learmont, Jennifer
McPhee, Dale A.
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NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Crowe, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COOPER, David
TITLE OF INVENTION: NON-F
NUMBER OF SEQUENCES: 800
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ADDRESSEE: Scully, SC
STREET: 400 Garden Ci
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APPLICANT: Deacon,
APPLICANT: Learmon
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STATE:
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               TGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG
                                                                                                                        TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA
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                                                                                                        ACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG
                                                                                                                                                            ACTICCGCGAGCTGAACAAGCGCACCCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCC
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                                                                    AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT
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TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-388-353-1 Query Match
Best Local Similarity 67.7%;
Matches 1606; Conservative 2116 131 365 419 539 719 779 839 1997 191 2057 251 311 629 g pp g g a QQ δ g ò g g g q g g ò ò g ò ò à ò ò δ δ ò ò

1426 1486 1546 1846 3075 3375 3615 1907 TCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGAGAGCCCATCATCG 1966 1366 1139 GCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC 1198 2776 ATTICAGAGAACTTAATAAGAGAACTCCAAGATTICTGGGAAGTTCAATTAGGAATACCAC 1019 TCAGCGTGCCCCTGGACGAGTTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCA 3016 CACCAGCAATATTCCAGTGTAGCATGACAAAATCTTAGAGCCTTTTAGAAAAACAAAATC 3136 GGCAGCATAGAACAAAAATAGAGGAACTGAGACAACATCTGTTGAGGTGGGGATTTACCA TGCGCCAGCTGTGCAAGCTGCGCGCGCGCCCAAGGCCCTGACCGACATCGTGCCCCTGA 3436 CAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAGATTCTAAAAGAACCGGTACATG 3496 GAGTGTATTATGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGGGCAAGGCC 1667 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1787 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGG ACTICCGCGAGCTGAACAAGCGCACCCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCC 959 ACCCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACT 2836 ATCCTGCAGGGTTAAAACAGAAAAATCAGTAACAGTACTGGATGTGGGCGATGCATATT CCGAGATCGTGATCTACCA - - - - - - GGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCG 123 GCCAGCACCGCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCTGCGGTGGGGCTTCACCA 1313 CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCAT-----CGAGCTGCACC CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACG CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGGAGACCGGTGCACG GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 1727 AGATGCGCACCGCCCACACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG 3676 CCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAATTACCCATACAAAAGG 1847 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGT 1079 3256 3316 1487 2716 899 1199 1367 1427 1547 1607 3736 g qq g qq Op g g g Db g g g qq рp Q δy ò ò ò g δy ö δy δ δy Qγ δ δ δ δy Pb δ Qγ ò δy

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                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2358
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
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FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: FRANK S DIGIGLIO REFERENCE/DOCKET NUMBER: 9606Z TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08488551B Patent No. 6015661
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ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DX
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17-MAY-1995
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APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : (516) 742-4343
(516) 742-4366
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U.S.A.
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                                                                                                                                                               43.8%; Score 1075.2; DB 3; Length 9709;
67.7%; Pred. No. 5.1e-168;
Live 0; Mismatches 738; Indels 28;
               SEQUENCE CHARACTERISTICS:
LENGTH: 9709 base pairs
                                                                                                                                                                                                    Matches 1606; Conservative
INFORMATION FOR SEQ ID NO:
                                                                         single
                                                    TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                   Similarity
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                                                                                                                           US-08-488-551B-1
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                     959 ACCCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGCGGCGACGCCTACT
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TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
FILE REFERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT PILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                             2267 TGCCCGCCCACAAGGGCATCGGCGCCAACGAGCAGATCGACAAGCTGGTGAGAGGGCA
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                                                               GCTACGTGACCGACCGGGCCCGCAGAAGATCGTGAGCCTGACCGAGACCACCAGA
                                                                                                       3916 GATATGTAACTGACAGAGGAAGACAAAAAGTTGTCCCCCTAACGGACACAACAAATCAGA
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67.7%; Pred. No. 5.1e
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GCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCA
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Sequence 13, Application US/08935312 Patent No. 6207455 GENERAL INFORMATION: APPLICANT: CHANG, Lung-Ji

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                                                                                                                                                        COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                           E: BROWDY AND NEIMARK, P.L.L.C. 624 Ninth Street, N.W.
TITLE OF INVENTION: LENTIVIRAL VECTORS NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERCE/DOCKET NUMBER: CHANG-112
TELECOMMUNICATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,312
FILING DATE: 22-5EP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = ""DNA""
US-08-935-312-13
                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                            ZIP: 2001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12494 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                    CITY: Washington STATE: D.C.
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Matches 1606; Conserv
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                                                                                            AGATGCGCACCGCCCACAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG 1786
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                                                                       AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA
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TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saliwanchik, Lloyd & Saliwanchik
21 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2421 N.W. 41st Street, CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/08848760B Patent No. 6248721 GENERAL INFORMATION:
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2087 AAGTAGGACAGTATGATCAGATACTCATAGAAATCTGCGGACATAAAAGCTATAGGTACAG 2146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 GCAACTGCCGCGCCCCCCCCGCAAGAAGGCCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGA 190
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SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 5.2e-168;
                                           APPLICATION NUMBER: US/08/848,760B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CNG-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                    APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                                                                                TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                   FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: /desc = "DNA
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12494 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                              NAME: PACE, DORAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.8%;
67.7%;
                                                                                                                PRIOR APPLICATION DATA:
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Matches 1606; Conservative
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| QQ | 2207 | CATTAGTCCTATTGAGACTGTACCAGTAAAATTAAAGCCAGG | 992 |
| Qy Db | 719 | TGGACGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCG 77 | 78 326 |
| Oy Dp | 779 | CCATCTGCGAGGAGATGGAGAAGGGCAAGATCACCAAGATCGGCCCGGAGAACCCCT 83 | 38 |
| Qy | 839 | CACCCCCGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG 8 | , ω - |
| Qy | 89 | TICCGCGAGCTGAACAACGCCCCAGGACTTCTGGGAGGTGCAGCTGGGGCATCCCC 9 | * & C |
| Qy | 959 | ACT 10 | 1 9 |
| Qy | 1019 | AGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA | 5 0 |
| Qy Db | 1079 | CA 11 AT 26 | 138 |
| Qy Dp | 1139 | ACCAAGATCCTGGAGCCTTCCGCGCCCGCAACC 11 | 9 4 |
| Qy Db | 1199 | CAGCGACCTGGAGATCG 12 | 50 |
| Qy | 1253 | TCACCA 13 TACCA 28 | 312 |
| Qy Db | 1313 2867 | -CGAGCTGCACC 13 1 ATGAACTCCATC 29 | 366 926 |
| Qy Db | 1367 | 14 | 126 986 |
| Oy Db | 1427 2987 | 3 14 3 30 | 8 4 |
| Qy Db | 3047 | 15. 31. | 4 0 |
| Qy Dp | 1547 | CG 16 | 0 9 |
| Qy Db | 1607 3167 | 16 | 566 |
| Q. Dp | 1667 | AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 17; | 726 |

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1727 AGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCG 1786
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Patent No. 6027881
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Stauber, Roland H.
APPLICANT: Stauber, Roland H.
APPLICANT: Wournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
                  3707 TGACAGACTCACAATATGCATTGGGAATCATTCAAGCACAACCAGATAAGAGTGAATCAG
                                                                               1967 GCGCCGAGACCTTCTACGTGGACGCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCG
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                                                                                                                           1847 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGGAGTGGGAGT
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                                                              1787 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG
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San Francisco
California
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APPLICATION NUMBER: US/08/646,538
FILING DATE: No. 6027881 yet assigned
CLASSIFICATION: 435
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-646-538-35
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STATE:
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                                                                                                                                                                                                                                                                                               DB 3; Length 15581
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                            43.8%; Score 1075.2; DB 3; 67.7%; Pred. No. 5.3e-168; Live 0; Mismatches 738;
                                           015280-249000
                                                                                                                                                                                                                                  LOCATION: 1..15581
COTHER INFORMATION: /note= "pNLnSG11"
US-08-646-538-35
         NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 01526
TELECHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 15581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.7 Matches 1606; Conservative
                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                              Query Match
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                                                                                              1313 CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCAT-----CGAGCTGCACC
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                                                                     779 CCATCTGCGAGGAGATGGAGAAAGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCT
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3676 CCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAATTACCCATACAAAGG 3735
                                          1847 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCCGAGTGGGAGT 1906
                                                                                                                         TCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCCATCATCG 1966
                                                                                                                                            3856 GAGCAGAAACTTTCTATGTAGATGGGGCAGCCAATAGGGAAACTAAATTAGGAAAAGCAG 3915
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APPLICANT: Pavlakis, George N.
APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
                                                               2087 AGACCGAGCTGCAGGCCATCCAGCTGGCCGTGCAGGACAGCGGCAGCGAGGTGAACATCG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/503,222
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Patent No. 6265548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3'CORRESPONDENCE ADDRESS:
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STATE: California
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CITY: Sa
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                                                                                                                                                                                                                                                                                                      Length 15581;
                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                  43.8%; Score 1075.2; DB 4;
67.7%; Pred. No. 5.3e-168;
tive 0; Mismatches 738;
015280-249000
                                                                                                                                                                                                                            LOCATION: 1..15581
COTHER INFORMATION: /note= "pNLnSG11"
US-09-503-222-35
                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION
                                                                                                     LENGTH: 15581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 67.7 Matches 1606; Conservative
                                                                                                                                          single
                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                             MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                      Query Match
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SOFTWARE: Patentin Ver. 2.0
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US-08-944-449-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7
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 CCATCTGCGAGGAGATGGAGGAGGGGGAAGATCACCAAGATCGGCCCCGAGAACCCCT
                   2656 AAATTTGTACAGAAATGGAAAGGAAGGAAAATTTCAAAAATTGGGCCTGAAAATCCAT
                                                                                      ACTICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
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                                           ACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGG
                                                                                                                                  ACCCGGCCGGCCTGAAGAAGAAGAGGCGTGACCGTGCTGGACGTGGGCGACGCCTACT
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APPLICANT: KURTH, REINHARD
APPLICANT: BATER, MICHAEL
APPLICANT: METERNE, KARIN
APPLICANT: METERNE, KARIN
TITLE OF INVENTION: Use of an "immunodeficiency-virus suppressing
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmphokine (ISL)" to inhibit the replication of
TITLE OF INVENTION: Upmper: particularly of retroviruses
CURRENT FILING DATE: 1997-10-06
EARLIER FILING DATE: 1995-08-18
EARLIER FILING DATE: 1995-08-18
EARLIER FILING DATE: 1995-04-07
NUMBER OF SEQ ID NOS: 8
4096 AGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAGGAAAAAGTCTACCTGGCATGGG
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; Patent No. 5985613
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| TANGGANCCAAAGAAAGACCTGTTAAAGTGTTTCAATTGTGGCAAAGAAGAGGGCACACGAGGAAGAAGACCCAAAGAAAGAAAGACCCCCC | 4 |
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1312 1486 1546 1606 1666 3562 1726 1786 1846 3862 4042 2266 4162 3262 1426 3322 3622 3922 3623 GGATGAGGGGTGCCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAAAGTAT 3682 CCGAGATCGTGATCTACCA-----GGCCCCCTGTACGTGGGCAGCGACCTGGAGATCG 1252 3383 TAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAA 3323 ACATACAGAAGTTAGTGGGAAAATTGAATTGGGCAAGTCAGATTTATGCAGGATTAAAG 1547 CCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACG 1667 AGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 1727 AGAIGCGCACCGCCCACACCAACGACGIGAAGCAGCIGACCGAGGCCGIGCAGAAGAICG 3683 CCACAGAAAGCATAGTAATATGGGGAAAGATTCCTAAATTTAAACTACCCATACAAAGG 1907 TCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGGAGGCCCATCATCG 3923 GATATGTTACTGACAGAGGAAGACAAAAAGTTGTCTCCATAGCTGACACAAATCAGA AGACTGAATTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAAACATAG 4043 TAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAAACCAGATAAGAGTGAATCAG AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG 1313 CCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCAT-----CGAGCTGCACC CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACG 1487 IGGGCCAGCTGTGCAAGCTGCTGCGGGGGCGCCAAGGCCCTGACCGACATCGTGCCCTGA 1607 GCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACC 1787 CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG 1847 AGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCCGAGTGGGAGT GCGCCGAGACCTTCTACGTGGACGCCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCG GCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGA AGACCGAGCTGCAGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCG TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCG GCCAGCACCGCGCCCAAGATCGAGGAGCTGCGGCAAGCACCTGCTGCGGGCTTCACCA 3863 2027 3983 2147 2207 4103 1199 1253 1367 1427 1961 2087 Db Q Dp Db δ g Op QΥ q δý QQ D d q q g qq Dp QΥ g QΥ g δy qq $^{\circ}$ à ŏ δ δ δ Ω δ Óγ ò Óλ

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                                4163 TACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAA 4222
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Pred. No. 1.9e-166;
0; Mismatches 744;
                                                                    TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2358
                                                                                       4223 TCAGGAAAGTACTATTTTGAATGGAATAGAT 4254
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APPLICATION NUMBER: DE 195 13 152.5
FILING DATE: 07-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P8341-9012
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/353,362
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      Sequence 7, Application US/09353362
Patent No. 6383739
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P8:
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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ilarity 67.5%;
Conservative
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 9737 base pairs
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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US-09-353-362-7
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                                                                                                        2723 ACAATACTCCAGTATTTGCTATAAAGAAAAAAGACAGTACTAAATGGAGAAAACTAGTAG
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                                               CCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACG
                                    ACATCCAGAAGCTGGTGGCCAAGCTGGGCCAGCCAGATCTACCCCGGCATCAAGG
        3503 AAGTATATGACCCATCAAAAGACTTAGTAGCAGAAATACAGAAGGCAGGGGCAAGGCC
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Search completed: February 10, 2003, 20:51:07 Job time : 166.805 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

February 10, 2003, 12:45:48; Search time 107.404 Seconds (without alignments) 10843.369 Million cell updates/sec Run on:

US-09-610-313-32

1 gtcgacgccaccatggccga......gggctagcaccggtgaattc 2457 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

408267 seqs, 237001491 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Published_Applications_NA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | ! | sednence 7, Appli | Sequence 6, Appli | Sequence 1, Appli | 3, | 7 | Sequence 9, Appli | 11, | Т | 1, A | 1 | 3, | Sequence 4, Appli | 6 | Sequence 4, Appli | Sequence 5, Appli | l, A | Sequence 56, Appl | Sequence 56, Appl | 56, |
|-------------------------------|--------|-------------------|-------------------|-------------------|-----------------|-----------------|-------------------|------------------|------------------|-----------------|------------------|-----------------|-------------------|-----------------|-------------------|-------------------|-----------------|-------------------|-------------------|------------------|
| QI | | 05-09-999-183-2 | US-09-872-733-6 | US-09-872-733-1 | US-09-872-733-3 | US-09-735-487-7 | US-09-735-487-9 | US-09-735-487-11 | US-09-735-487-13 | US-09-999-183-1 | US-09-737-190A-1 | US-09-943-286-3 | US-09-943-286-4 | US-09-943-286-9 | US-09-798-675-4 | us-09-798-675-5 | us-10-097-997-1 | US-09-886-156-56 | us-09-886-150-56 | US-09-886-149-56 |
| 80 | | 7 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 6 | 6 | 6 | 6 |
| % Query Match Length DB | 1000 | 4 20/ | 8366 | 4338 | 2467 | 2601 | 2601 | 2601 | 2601 | 4307 | 9719 | 8933 | 8933 | 8933 | 9544 | 9918 | 2348 | 9793 | 9793 | 9793 |
| % Query Match | 4 30 | 4.00 | 62.6 | 61.2 | 46.3 | 44.0 | 44.0 | 44.0 | 44.0 | 44.0 | 44.0 | 41.9 | 41.9 | 41.9 | 41.6 | 41.6 | 33,3 | 32.8 | 32.8 | 32.8 |
| Score | 1607 4 | *· / OOT | 1539.2 | 1503.8 | 1137 | 1081.6 | 1081.6 | 1081.6 | 1081.6 | 1081.6 | 1081.6 | 1029.2 | 1029.2 | 1029.2 | 1022.8 | 1022.8 | 818.4 | 805.8 | 805.8 | 805.8 |
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ALIGNMENTS

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1086 CCTGGCTGAGGCCATGAGCCAGTGCGACTCGCTACCATCATGATGCAGCGCGGCAA 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Codon optimised gagpol sequence
US-09-999-183-2
                                                                                   GENERAL INFORMATION:
APPLICANT: MITROPHANOUS, et al
ITLE OF INVENTION: In Vivo Selection Method
FILE REFERENCE: 674523-2009
CURRENT APPLICATION NUMBER: US/09/999,183
CURRENT APPLICATION NUMBER: US/09/999,183
CURRENT APPLICATION NUMBER: DCT/GB00/02136
PRIOR APPLICATION NUMBER: 9912965.2
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: SeqWin99
                                             Sequence 2, Application US/09999183 Patent No. US20020147169A1
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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RESULT 1
US-09-999-183-2
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                                      2525 CGACATACAGAAGCTGGTGGGGAAGTTGAACTGGGCCAGTCAGATTTACCCAGGGATTAA
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tive 0; Mismatches 448; Indels 28;
                   Sequence 6, Application US/09872733
Patent No. US20010036655A1
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                            2456 TATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACCCAGATCGGCT
                                                                           2516 GCACCTTGAACTTCCCCATCAGCCCTATTGAGACGGTGCCCGTGAAGTTGAAGCCGGGGA
                                                                                                                                           2696 ACAACACTCCCAGTCTTCGCAATCAAGAAGAAGGACAGTACCAAGTGGAGAAAGCTGGTGG
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TGCTGATCGGCCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCT
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APPLICANT: The Government of the United States of America, as TITLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND TITLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG ENV CURRENT FILE REFERENCE: 2026-4287051 HIV GAG/POL, SIV GAG & ENV CURRENT APPLICATION NUMBER: US/09/872,733
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VET. 2.1
3536 AATGGACCTACCAATCTACCAGGAGCCCTTCAAGAACCTGAAGACAGGCAAGTACGCAA 3595
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                                                                                                                                        GAGCAGAGACCTTCTACGTGGATGGGGCAGCCAACAGGGAGACCAAGCTGGGCAAGGCAG
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OTHER INFORMATION: Immunodeficiency Virus - 1 Gag/Pol gene
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HIV GAG/POL,
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GENERAL INCORNATION:
APPLICANT: The Government of the United States of Amerititle OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV CITLE OF INVENTION: SIV ENV GENES
FILE REFERENCE: 2026-4287US1 HIV GAG/POL, SIV GAG & ENV CURRENT APPLICATION NUMBER: US/09/872,733
CURRENT FILING DATE: 2001-06-01
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 1999-12-23
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SOFTWARE: Patentin Ver. 2.1
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Sequence 7, Application US/09735487

Sequence 7. Application US/09735487

Patent No. US20020042679A1

GENERAL INFORMATION:

APPLICANT: HERTOGS, Kurt

APPLICANT: POWNELS, Rddi

TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY

TITLE OF INVENTION: HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY

FILE REFERENCE: 1377-125P

CURRENT APPLICATION NUMBER: US/09/735,487

CURRENT FILING DATE: 1098-07-24

PRIOR FILING DATE: 1998-07-24
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Pred. No. 6.4e-170;
0; Mismatches 734;
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; OTHER INFORMATION: gag Polyprotein
US-09-735-487-7
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Best Local Similarity 67.9%;
Matches 1610; Conservative
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                                                          CAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATTCTAAAAGAACCAGTACATG
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APPLICANT: de BETHUNE, Marie-Pierre APPLICANT: HERTOGS, Kurt APPLICANT: PAUWELS, Rudi TITLE OF INVENTION: METHOD OF MANAGI TITLE OF INVENTION: HIV POSTITIVE BR TITLE OF INVENTION: OF HUMAN HIV STF Sequence 9, Application US/09735487 Patent No. US20020042679A1 GENERAL INFORMATION: US-09-735-487-9

METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY OF HUMAN HIV STRAINS

FILE REFERENCE: 1377-125P CURRENT APPLICATION NUMBER: US/09/735,487

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44.0%; Score 1081.6; DB 10

Best Local Similarity 67.9%; Pred. No. 6.4e-170;

Matches 1610; Conservative 0; Mismatches 734;
             09/117,217
                                                                                                                                                      LOCATION: (334)...(489)
OTHER INFORMATION: gag P6 (52 AA)
CURRENT FILING DATE: 2000-12-14
           PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
                                                     Patentin Ver. 2.0
                                                                                                             ORGANISM: HIV-HXB2
                                                                                                                                         NAME/KEY: CDS
                                                                                 2601
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                                                   SOFTWARE:
SEQ ID NO 9
                                                                                                 TYPE: DNA
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Sequence 11, Application US/09735487

Patent No. US20020042679A1

GENERAL INFORMATION:
APPLICANT: HERTOGS, Kurt
APPLICANT: HERTOGS, Rudi
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILLS REPERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/735,487

CURRENT FILING DATE: 1098-07-24
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44.0%; Score 1081.6; DB 1
Best Local Similarity 67.9%; Pred. No. 6.4e-170;
Matches 1610; Conservative 0; Mismatches 734;
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; OTHER INFORMATION: Protease
US-09-735-487-11
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SOFTWARE: PatentIn Ve
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Sequence 13, Application US/09735487 Patent No. US20020042679A1 GENERAL INFORMATION:
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Matches 1610; Conservative
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                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: HIV-HXB2
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LENGTH: 2601
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APPLICANT: de BETHUNE, Kurt
APPLICANT: HERTGGS, Kurt
APPLICANT: HERTGGS, Kurt
APPLICANT: HERTGGS, Kurt
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: OF HUMAN HIV STRAINS
TITLE OF INVENTION: OF HUMAN HIV STRAINS
CURRENT APPLICATION NUMBER: US/09/735,487
CURRENT FILING DATE: 200-12-14
PRIOR PAPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
                         2356 TACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAA 2415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (750)..(2435)
: OTHER INFORMATION: Reverse Transcriptase
US-09-735-487-13
                                                                                                                                 2416 TCAGGAAAGTACTATTTTAGATGGAATAGAT
                                                                              2327 TCCGCAAGGTGCTGTTCCTGGACGGCATCGAT
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                                          CCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGG
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Patent No. US20020147169A1
GENERAL INFORMATION:
APPLICANT: MITROPHANOUS, et al
TITLE OF INVENTION: In Vivo Selection Method
FILE REPERENCE: 674523-2009
CURRENT APPLICATION NUMBER: US/09/999,183
CURRENT FILING DATE: 2001-11-29
PRIOR PAPLICATION NUMBER: PCT/GB00/02136
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Seqwin99
SEQ ID NO 1
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                                         Length 4307
                                                           28;
                                      Score 1081.6; DB 10; Lengt
Pred. No. 6.5e-170;
0; Mismatches 734; Indels
          Human immunodeficiency virus type
                                       44.0%;
                                     Query Match
Best Local Similarity 67.99
Matches 1610; Conservative
                   US-09-999-183-1
TYPE: DNA ORGANISM:
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TITLE OF INVENTION: A Method for Changing a Target Array, a Method for Analyzing
TITLE OF INVENTION: A Structure, and an Apparatus, a Storage Medium and a
TITLE OF INVENTION: Transmission Medium Therefor
FILE REPERBNCE: JP919990270051 (40043)
CURRENT APPLICATION NUMBER: US/09/737,190A
CURRENT FILING DATE: 2000-12-14
SOFTWARE: PATENTING VET: 2.1
SEQ ID NO 1
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                        AGACCGAGCTGCAGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCG
                                       2057 TGAAAGATTGTACTGAGAGACAGGCTAA-TTTTTAGGGAAGATCTGGCCTTCCTACAAG
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Matches 1610; Conserv
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2236 CIGIATCCTTTAACTTCCCTCAGGTCACTCTTTGGCAACGACCCCTCGTCACAATAAAGA 2295
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                     3376 TAAGGCAATTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAA 3435
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Db 4216 TCAGGAAGTACTATTTTAGATGGATAGAT 4247

RESULT 11

Sequence 3, Application US/09943286

Patent No. US20020106668A1

Patent No. US20020106668A1

TGENERAL INFORMATION:

APPLICANT: NUNDOMURA, KIYOtada

TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD

FILE REFERENCE: GP104-02.UT

CURRENT FILING DATE: 2001-08-30

NUMBER OF SEQ ID NOS: 9
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                                                                                                                           of transcripts produced from the BH10
                                                                                                                                                                                        DB 10; Length 8933;
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                                                                                                                                                                                      Query Match 41.9%; Score 1029.2; DB 10. Best Local Similarity 55.2%; Pred. No. 2.8e-161; Matches 1329; Conservative 277; Mismatches 738;
SOFTWARE: FastSEQ for Windows Version 3.0
                                             TYPE: RNA
ORGANISM: Human Immunodeficiency Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 GCAAGGCCCGCGAGT-------
                                                                                                                        OTHER INFORMATION: Sequence;
OTHER INFORMATION: plasmid.
US-09-943-286-3
                                                                                                           ...(8933)
                                                                                           NAME/KEY: source LOCATION: (1)...
                              LENGTH: 8933
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                                                    983 AGAGCGTGACCGTGCTGGACGTGGCCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACT
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                                  AGCTGTGGTACCAGCTGGAGAGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACG 1990
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3119 AGUAUUGGCAAGCCACCUGGAUUCCUGAGUGGGAGUUUGUUAAUACCCCUCCUUUAGUGA 3178
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                                                                                                          Query Match 41.9%; Score 1029.2; DB 10; Length 8933; Best Local Similarity 55.2%; Pred. No. 2.8e-161; Matches 1329; Conservative 277; Mismatches 738; Indels 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nunomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02.UT
CURRENT APPLICATION NUMBER: US/09/943,286
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
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: LOCATION: (4135)...(4155)
OTHER INFORMATION: Mutated
: OTHER INFORMATION: 4152-3,
US-09-943-286-4
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US-09-943-286-4
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| Qy Db | 191 | TGAAGGACTGCACCGAGCCCAGGCCAACTTCTTCCGCGAGGACCTGCCCTTCCCCCAGG 250 | 38 |
| ολ | 251 | 27 | 4 |
| g | 1439 | GGAAGGCCAGGGAAUUUUCUUCAGAGCAGACCAGAGCCAACAGCCCCACCAUUUCUUCAG 149 | 86 |
| Qy Dp | 275 | AGCAGAACCGCGCCAACAGCCCCACCAGCGGGGGTGCAGGTGCGCGGCGACA 328 | .58 5.88 |
| Qy | 329 | ACCCCGCAGGAGGCGGCGGCGGCGAGGGCACCCTGAACTTCCCCCAGA 382 | 18 |
| Oy Dp | 383 | 44 | 2 7 8 |
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| oy Dp | 503 1739 | 56 | 2 6 |
| Qy Db | 563 1799 | 62 | 2 2 2 |
| Qy Db | 623 | ACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCTGAACTTCCCCATCAGCC 682 | 2 18 |
| Qy Dp | 683 1919 | CCATCGAGACCGTGCCCGTGAAGCTGAAGCCGGCATGGACGCCCCAAGGTGAAGCAGT 742 1: | 2 78 |
| Qy Db | 743 | GGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGG 802 | 38 |
| Qy | 803 | 86 | 2 98 |
| Qy Db | 863 | AGAAGAAGGACAGCAACGAAGGGGAAGCTGGTGGACTTCCGGGAGCTGAACAAGGGG 922 | 2 58 |
| Qy Db | 923 | CCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCGCGGCCTGAAGAAGA 982 1 1 1 1 1 1 1 1 1 | 2 18 |
| Qy | 983 | AGAGCGTGACCGTGCTGGACGCGACGCCTACTTCAGCGTGCCCCTGGACGACGACT 104 | 42 |
| Qy Db | 1043 2279 | 11 | 02 38 |
| Qy Db | 1103 | ACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCAGCCCCAGCATCTTCCAGAGCAGCA 116 1 1 1 1 1 1 1 1 1 | 62 98 |
| Qy Dp | 1163 | TGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATCTACCA 121 | 17 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (4140)...(4159)
OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152,
OTHER INFORMATION: 4156-57, 4159
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                                                                                                                                                                                                                                               APPLICANT: Unnomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: 6P104-02.UT
CURRENT APPLICATION NUMBER: US/09/943,286
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                   ACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTACCAGG
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FILE REFERENCE: E056 2020
CURRENT APPLICATION NUMBER: US/09/798,675
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
SPRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
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US-09-798-675-4
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OTHER INFORMATION: Construct of vaccine vector pGA2 and insert JS2 expressing cla OTHER INFORMATION: HIV-1 VL
                                                                                                                    OTHER INFORMATION: encoding inner core protein NAME/EXEX: misc_feature LOCATION: (1401)..(3617) OTHER INFORMATION: encoding viral rproteins including reverse transcriptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 TGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCGTGA 622
                                                                                                                                                                                                                                                                                                  Rev regulating transfer of RNA to cytoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 TCACCCTGTGCGCCCCCCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742; Indels
                                                                                                                                                                                                                                        high level of virus particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1022.8; DB 1
Pred. No. 3.2e-160;
0; Mismatches 742;
                                                                                                                                                                                                                                                                           LOCATION: (3847)..(6518)
OTHER INFORMATION: encodes Rev regulating NAME/KEY: misc_feature
LOCATION: (4102)..(6660)
OTHER INFORMATION: encoding ADA Env NAME/KEY: misc_feature
LOCATION: (6672)..(5544)
OTHER INFORMATION: Vaccine vector pGA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.68;
66.58;
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     LOCATION: (3708)..(6334)
OTHER INFORMATION: induces
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Matches 1602; Conservative
                                                                              NAME/KEY: misc_feature
LOCATION: (106)..(1641)
                                                                                                                                                                                                   NAME/KEY: misc-feature
                                                                                                                                                                                                                                                             NAME/KEY: misc-feature
LOCATION: (3847)..(651)
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| 972 803 032 | GGCCATTGACAGAAGAAAAAAAGCATTAGTAGAAAATTTGTACAGAAAAGG AGGGCAAGATCACCAAGATCGGCCCCGAGAACCCTACAACACCCCCGTGTTCGCCATCA | 2031 |
| | AGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGTGAACAAGCGCA | 922 |
| | CCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCACCCGGCCGG | 982 |
| | AGAGCGTGACCGTGCACGCGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACT | 1042 |
| | TCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCT | 1102 2331 |
| | ACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCAGCCCCAGCATCTTCCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC | 1162 |
| | | 1217 |
| | -GGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGCCCAGCACCGCGCCAAGATCGAGG : | 1276 2511 |
| | AGCIGCGCAAGCACCIGCIGCGCTGGGGCTTCACCACCCCGGCAAGAAGCACCAGAAGG : | 1336 2571 |
| | AGCCCCCTTCCTGCCCATCGAGCTGCACCGGACAGTGGACCGTGCAGCCC : | 1390 2631 |
| | TCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCAAGC : | 1450 2691 |
| _ | | 1510 2751 |
| | GCGGCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGGGGCGGGC | 1570 2811 |
| • • | CCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCAGCGGGTGTACTACGACCCCAGCAAGG | 1630 |
| ~ ~ | ACCIGGIGGCCGAGAICCAGAAGCAGGGCCACGACCAGGGGACCTACCAGTICTACCAGG 1 | 1690 2931 |

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OTHER INFORMATION: Construct of vaccine vector pGAl and vaccine insert expressing OTHER INFORMATION: ade B HIV-1 Gag-Po NAME/KEY: misc_feature
1691 AGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCACCAACG 1750
                                                                       1751 ACGIGAAGCAGCIGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGG 1810
                                                                                                                                               1811 GCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCG 1870
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                     2932 AGCCATTTAAAAATCTGAAAAGGGAAAATATGCAAGAATGAGGGGTGCCCACACTAATG 2991
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                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HIV VACCINES
FILE REFERENCE: E056 2020
CURRENT APPLICATION NUMBER: US/09/798,675
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
NUMBER PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/09798675
; Patent No. US20020106798A1
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US-09-798-675-5
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LUCATION: (3847)...(5944)
OTHER INFORMATION: encodes protein regulating the transfer of RNA to cytoplasm NAME/KEY: misc_feature
LOCATION: (3939)...(4181)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 TCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 GCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGA 190
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                                                                                                                                                                                                                                                             LOCATION: (3939)...(4181)

LOCATION: (3939)...(4181)

OTHER INFORMATION: gene participates in viral assembly and budding NAME/KEY: misc_feature

LOCATION: (4099)..(4941)

OTHER INFORMATION: encodes truncated form of viral coat protein MAME/KEY: misc_feature

LOCATION: (6098)..(9918)

OTHER INFORMATION: vaccine vector pGA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.6%; Score 1022.8; DB 10; Length 9918;
66.5%; Pred. No. 3.2e-160;
tive 0; Mismatches 742; Indels 64;
LOCATION: (106)..(1641)

OTHER INFORMATION: encodes proteins of viral inner core
NAME/KEY: misc_feature
LOCATION: (1401)..(3617)

OTHER INFORMATION: encodes viral proteins but not integrase
NAME/KEY: misc_feature
LOCATION: (3708)..(5715)

OTHER INFORMATION: equiates high-level production of HIV genes
NAME/KEY: misc_featre
LOCATION: (3847)..(5944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.5
Matches 1602; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 GCAAGGCCCGCGAGT----
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1691 AGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCACACAACG 1750
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                                                                                                                                                                                                                                                                                                                              1972 GGCCATTGACAGAAAAAAAAAAAAAGCATTAGTAGAAATTTGTACAGAAATGGAAAAGG 2031
                                                                                                                                                                                 2032 AAGGGAAATTTCAAAAATTGGGCCTGAGAATCCATACAATACTCCAGTATTTGCCATAA 2091
                                                                                                                                            803 AGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCA 862
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683 CCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCCATGGACGCCCCCAAGGTGAAGCAGT
                                                                       743 GGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGG
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          2992 AIGTAAAAAATTAACAGAGGCAGTGCAAAAATAACCACAGAAAGCATAGTAATAIGGG 3051
                                             3052 GAAAGACTCCTAAATTTAAACTACCCATACAAAGAGAAACATGGGAAACATGGGGCAG 3111
                                                                                  TGGCCCTGCAGGACAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGG 2170
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